

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:29:28 ; Search time 0.001 Seconds
(without alignments)
241.650 Million cell updates/sec

Title: US-09-817-538-2
Perfect score: 1611
Sequence: 1 atgtctgggtctctgcgcg.....tccctcagctttttttccccc 1611

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 75 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : rst2.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
C 1	28	1.7	28 1	H22321
C 2	25	1.6	25 1	AA469268
C 3	19.4	1.2	22 1	AA921198

ALIGNMENTS

RESULT 1
H22321/c
LOCUS
DEFINITION
H22321
Y13609.r1 Soares breast 3NHBst Homo sapiens cDNA clone
IMAGE:160337 5' similar to SP:RS5_RAT P24050 40S RIBOSOMAL PROTEIN
, mRNA sequence.
ACCESSION
H22321.1 GI:891016
VERSION
H22321.1
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 28)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
JOURNAL
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 798
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 798 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. 28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:574362"
/db_xref="taxon:9606"
/clone="IMAGE:160337"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares breast 3NHBst"
/notes="Organ: Breast; Vector: pTV73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pTV73 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

Query Match 1.7% Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred No. 0.39; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0

Qy 19 CGCTGGTGGTCTGCTCTCCCACTCGGTC 46
|||
Db 28 CGCTGGTGGTCTGCTCTCCCACTCGGTC 1

RESULT 2

AA469268/c
LOCUS
DEFINITION
AA469268
nc68a03.81 NCI CGAP P1 Homo sapiens cDNA clone IMAGE:771724
similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5. i, mRNA
sequence.
ACCESSION
AA469268.1 GI:2195802
VERSION
AA469268
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -41ml3 fwd. EF from Amersham

High quality sequence stop: 1.
Location/Qualifiers
1. .25

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:771724"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI COAP Pri"
/note="Vector: pAMP10; Site 1: Not1; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 0.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CGCTGCTGCTGCTCTCCACTCG 43
Db 25 CGCTGCTGCTGCTCTCCACTCG 1

RESULT 3

AA921198

LOCUS

DEFINITION

Y22f12 r1 Soares thymus 2NbMT Mus musculus cDNA clone
IMAGE:1327727 5' similar to SW:HIDA_MOUSE C09106 HISTONE
DEACETYLASE HD1. [3] SW:HIDA_MOUSE TR:092534 ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AA921198 22 bp mRNA linear EST 20-APR-1998
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through INL ; contact the
IMAGE Consortium (info@image.inl.gov) for further information.

MGI:687271

Trace considered overall poor quality

Possible reversed clone; similarity on wrong strand

Seq primer: -28m13 rev2 Et from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

FEATURES

source

/clone="IMAGE:1327727"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares thymus 2NbMT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5,
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

Query Match 1.2%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred.No. 1.9;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1098 TACAATGACTACTTTGAATAC 1118
Db 2 TACAACGACTACTTTGAATAC 22

Search completed: June 24, 2004, 10:29:28
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:25:52 ; Search time 1 Seconds
(without alignments)
3.783 Million cell updates/sec

Title: US-09-817-538-2
Perfect score: 1611
Sequence: 1 agtctgggtctctgcgcg.....tccctcacgattttttccccc 1611

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 73 seqs, 1174 residues

Total number of hits satisfying chosen parameters: 146

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 73 summaries

Database : rnpn2.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21.8	1.4	25	1	US-10-859-198-165232
C 2	19.4	1.2	21	1	PCT-US04-00035-43855
C 3	17.8	1.1	21	1	PCT-US04-00035-43856
C 4	17.4	1.1	19	1	US-10-708-951-20910
C 5	17.4	1.1	19	1	US-10-708-951-20910
C 6	16.8	1.0	21	1	PCT-US04-00035-12071
C 7	16.8	1.0	21	1	PCT-US04-00035-28225
C 8	16.8	1.0	21	1	PCT-US04-00035-28228
C 9	16.8	1.0	21	1	US-10-847-918-12383
C 10	16.6	1.0	17	1	PCT-US02-38147A-198
C 11	16.4	1.0	20	1	US-10-057-550C-27
C 12	14.4	0.9	16	1	US-10-138-674B-5827
C 13	14.4	0.9	17	1	PCT-US03-41025-86
C 14	14.4	0.9	17	1	US-10-138-674B-4754
C 15	14.4	0.9	17	1	US-10-138-674B-7632
C 16	14.4	0.9	17	1	US-10-138-674B-7632
C 17	13.8	0.9	17	1	US-10-364-412A-3345
C 18	13.8	0.9	17	1	US-10-364-412A-3342
C 19	13.8	0.9	17	1	US-10-364-412A-5702
C 20	13.8	0.9	17	1	US-10-364-412A-5749
C 21	13.8	0.9	17	1	US-10-138-674B-947
C 22	13.8	0.9	17	1	US-10-138-674B-2635
C 23	13.8	0.9	17	1	US-10-138-674B-4755
C 24	13.8	0.9	17	1	US-10-138-674B-4756
C 25	13.8	0.9	17	1	US-10-138-674B-4757
C 26	13.8	0.9	17	1	US-10-138-674B-4758
C 27	13.8	0.9	17	1	US-10-138-674B-5394
C 28	13.4	0.8	15	1	US-10-138-674B-7633
C 29	13.4	0.8	15	1	US-10-834-967-771
C 30	13.4	0.8	15	1	US-10-834-967-3951
C 31	13.4	0.8	15	1	US-10-364-412A-5002
C 32	13.4	0.8	15	1	US-10-364-412A-5050
C 33	13	0.8	13	1	US-10-834-967-3378
C 34	13	0.8	13	1	US-10-257-017B-145445

C 34	13	0.8	13	1	US-10-257-017B-145446	Sequence 145446,
C 35	13	0.8	13	1	US-10-257-017B-151965	Sequence 151965,
C 36	13	0.8	13	1	US-10-257-017B-151966	Sequence 151966,
C 37	13	0.8	15	1	US-10-708-951-20910	Sequence 20910, A
C 38	13	0.8	15	1	US-10-708-951-20910	Sequence 46339, A
C 39	12.8	0.8	16	1	US-10-708-951-21033	Sequence 21033, A
C 40	12.8	0.8	16	1	US-10-708-951-21033	Sequence 46804, A
C 41	12.8	0.8	16	1	US-10-364-412A-5277	Sequence 5277, Ap
C 42	12.8	0.8	16	1	US-10-364-412A-7505	Sequence 7505, Ap
C 43	12.8	0.8	16	1	US-10-364-412A-7832	Sequence 7832, Ap
C 44	12.8	0.8	16	1	US-10-364-412A-7834	Sequence 7834, Ap
C 45	12.8	0.8	16	1	US-10-364-412A-8959	Sequence 8959, Ap
C 46	12.8	0.8	16	1	US-10-138-674B-5988	Sequence 5988, Ap
C 47	12.6	0.8	13	1	US-10-257-017B-41893	Sequence 41893, A
C 48	12.6	0.8	13	1	US-10-257-017B-41894	Sequence 41894, A
C 49	12.6	0.8	13	1	US-10-257-017B-48345	Sequence 48345, A
C 50	12.6	0.8	13	1	US-10-257-017B-48346	Sequence 48346, A
C 51	12.6	0.8	13	1	US-10-257-017B-188275	Sequence 188275,
C 52	12.6	0.8	13	1	US-10-257-017B-188276	Sequence 188276,
C 53	12.4	0.8	14	1	US-10-708-951-31150	Sequence 31150, A
C 54	12.4	0.8	14	1	US-10-708-951-31150	Sequence 43411, A
C 55	12.4	0.8	15	1	US-10-796-280-67936	Sequence 67936, A
C 56	12.4	0.8	15	1	US-10-708-951-20715	Sequence 20715, A
C 57	12.4	0.8	15	1	US-10-708-951-22787	Sequence 22787, A
C 58	12.4	0.8	15	1	US-10-708-951-40578	Sequence 40578, A
C 59	12.4	0.8	15	1	US-10-708-951-45190	Sequence 45190, A
C 60	12.4	0.8	15	1	US-10-834-967-1542	Sequence 1542, Ap
C 61	12.4	0.8	15	1	US-10-834-967-4433	Sequence 4433, Ap
C 62	12.4	0.8	15	1	US-10-364-412A-1151	Sequence 1151, Ap
C 63	12.4	0.8	15	1	US-10-364-412A-1178	Sequence 1178, Ap
C 64	12.4	0.8	15	1	US-10-364-412A-3817	Sequence 3817, Ap
C 65	12.4	0.8	15	1	US-10-364-412A-3852	Sequence 3852, Ap
C 66	12.4	0.8	15	1	US-10-364-412A-4291	Sequence 4291, Ap
C 67	12.4	0.8	15	1	US-10-364-412A-4292	Sequence 4292, Ap
C 68	12.4	0.8	15	1	US-10-364-412A-5773	Sequence 5773, Ap
C 69	12.4	0.8	15	1	US-10-364-412A-5828	Sequence 5828, Ap
C 70	12.4	0.8	15	1	US-10-364-412A-6612	Sequence 6612, Ap
C 71	12.4	0.8	15	1	US-10-364-412A-6645	Sequence 6645, Ap
C 72	12.4	0.8	15	1	US-10-364-412A-8313	Sequence 8313, Ap
C 73	12.4	0.8	15	1	US-10-364-412A-8336	Sequence 8336, Ap

ALIGNMENTS

RESULT 1

US-10-859-198-165232/c
; Sequence 165232, Application US/10859198
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; APPLICANT: Murphy, Ellen
; APPLICANT: Whitley, Maryann
; TITLE OF INVENTION: Nucleic Acid Arrays for Detecting Multiple Strains of a Non-Viral
; FILE REFERENCE: 031896-014000 (AM101085)
; CURRENT APPLICATION NUMBER: US/10859198
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/475,871
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 282011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe sequence
US-10-859-198-165232

Query Match 1.4%; Score 21.8; DB 1; Length 25;

Best Local Similarity 92.0%; Pred. No. 1.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 334 TCTTGGCTCCATCCGTCAGATAA 358

```

Db      25  TCTTGGCGTACATCCGTACAGATAA 1
|||||
RESULT 2
PCT-US04-00035-43855/c
; Sequence 43855, Application PC/TUS0400035
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: PCT/US04/00035
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43855
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US04-00035-43855
Query Match      1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred No. 3.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      131  CCGGAGGAAAGTCTGTACTA 151
          |||||
Db      21  CCGGAGGAAAGTCGGTACTA 1

RESULT 3
PCT-US04-00035-43856/c
; Sequence 43856, Application PC/TUS0400035
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: PCT/US04/00035
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43856
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
PCT-US04-00035-43856
Query Match      1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      129  ACCCGAGGAAAGTCTGTAC 149
          |||||
Db      21  AACCGGAGGAAAGTCGGTAC 1

RESULT 4
US-10-708-951-20883/c
; Sequence 20883, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD

```


Best Local Similarity 75.0%; Pred. No. 11;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1533 GTCAGGAGGAGGCGCAAGTT 1552
Db 2 GUCAGGAGGAGGCGCAAAU 21

RESULT 7
PCT-US04-00035-28225
; Sequence 28225, Application PC/TUS0400035
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: PCT/US04/00035
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28225
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US04-00035-28225

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 AAGAACTCTTCAACTTCAA 1423
Db 2 AAGAACTCTTCAACTTCAA 21

RESULT 8
PCT-US04-00035-28228
; Sequence 28228, Application PC/TUS0400035
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: PCT/US04/00035
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28228
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US04-00035-28228

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 AAGAACTCTTCAACTTCAA 1423
Db 1 AAGAACTCTTCAACTTCAA 20

RESULT 9

US-10-847-918-12383/c
; Sequence 12383, Application US/10847918
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12383
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-12383

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 957 AAGTGTGTGGAATTGTCTCAA 976
Db 21 AAGTGTGTGGAATTGTCTCAA 2

RESULT 10
PCT-US02-38147A-198/c
; Sequence 198, Application PC/TUS0238147A
; GENERAL INFORMATION:
; APPLICANT: Cell-Matrix, Inc.
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; APPLICANT: Broek, Daniel
; APPLICANT: Brooks, Peter C.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: 66797-164 (IX 5532)
; CURRENT APPLICATION NUMBER: PCT/US02/38147A
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/995,529
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-38147A-198

Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.9;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCCA 1469
Db 17 AAAAAGAGAAAGAYCCA 1

RESULT 11
US-10-057-550C-27/c
; Sequence 27, Application US/10057550C
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression

```
; FILE REFERENCE: ISPH-0625
; CURRENT APPLICATION NUMBER: US/10/057,550C
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-057-550C-27
```

```
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1507 AGGAGGAGAGCCAGAG 1524
    |||||
Db 19 AGGAGGAGAGCCAGAG 2
```

```
RESULT 12
US-10-138-674B-5827
; Sequence 5827, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-5827
```

```
Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 517 CTGGGGGCTGCACCA 532
    |||||
Db 1 CUGGAGCCGACCA 16
```

```
RESULT 13
PCT-US03-41025-86
; Sequence 86, Application PC/TUS0341025
; GENERAL INFORMATION:
; APPLICANT: Sequenom, Inc.
; APPLICANT: Langdon, Maria L.
; APPLICANT: Nelson, Matthew Roberts
; APPLICANT: Reneland, Rikard Henry
; APPLICANT: Kammerer, Stefan M.
; APPLICANT: Braun, Andreas
```

```
; APPLICANT: Dennissenko, Mikhail F.
; APPLICANT: Atienza, Josephine M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF TYPE II
; FILE REFERENCE: 524592007340
; CURRENT APPLICATION NUMBER: PCT/US03/41025
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: 60/435,431
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/498,970
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/498,100
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/477,437
; PRIOR FILING DATE: 2003-06-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US03-41025-86
```

```
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1218 CTTAGAAATGCTCCGC 1233
    |||||
Db 2 CTTAGAAATGCTCCGC 17
```

```
RESULT 14
US-10-138-674B-4754
; Sequence 4754, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-4754
```

```
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 18;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 517 CTGGGGGCTGCACCA 532
    |||||
Db 1 CUGGAGCCGACCA 16
```

```
RESULT 15
US-10-138-674B-7632
; Sequence 7632, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
```

```

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MSH900-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/136,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-7632

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 18;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGGCTGGACC 531
Db 2 GCUGGAGCCGCGACC 17

RESULT 16
US-10-364-412A-3345
; Sequence 3345, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3345
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (696917)...(696933)
; OTHER INFORMATION: Chromosome = 7 Strand = positive ConnectronObjectNumber = 6259
US-10-364-412A-3345

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1293 GATGAGCAGCAGACGA 1309
Db 1 GATGATGACGATGACGA 17

RESULT 17
US-10-364-412A-3942/C
; Sequence 3942, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3942
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (347222)...(347238)
; OTHER INFORMATION: Chromosome = 14 Strand = negative ConnectronObjectNumber = 12372
US-10-364-412A-3942

Query Match      0.9%; Score 13.8; DB 1; Length 17;

```

```

Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1293 GATGAGCAGCAGACGA 1309
Db 17 GATGATGACGATGACGA 1

RESULT 18
US-10-364-412A-5702/C
; Sequence 5702, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5702
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (394472)...(394488)
; OTHER INFORMATION: Chromosome = 7 Strand = negative ConnectronObjectNumber = 580
US-10-364-412A-5702

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1293 GATGAGCAGCAGACGA 1309
Db 17 GATGATGACGATGACGA 1

RESULT 19
US-10-364-412A-5749/C
; Sequence 5749, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5749
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (576156)...(576172)
; OTHER INFORMATION: Chromosome = 11 Strand = positive ConnectronObjectNumber = 939
US-10-364-412A-5749

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1293 GATGAGCAGCAGACGA 1309
Db 17 GATGATGACGATGACGA 1

RESULT 20
US-10-138-674B-947
; Sequence 947, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James

```

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 947
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-947

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 59.8%; Pred. No. 23;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGTGTGAACTT 482
DB 1 CAACUGCUUGAAACUU 17

RESULT 21
US-10-138-674B-2635/c
; Sequence 2635, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2635
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674B-2635

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGTGGTGTGCTGTC 34
DB 17 CTGCTGGTGTGCTGTC 1

RESULT 22
US-10-138-674B-4755
; Sequence 4755, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4755
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-4755

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 23;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCGCTGCACCATG 534
DB 1 UGGAGCCUGCACCACAA 17

RESULT 23
US-10-138-674B-4756
; Sequence 4756, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4756
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-4756

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 23;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 521 GGGCGTGCACCATGCAA 537
DB 1 GAGCCUGCACCACAA 17

RESULT 24
US-10-138-674B-4757
; Sequence 4757, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4757
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-4757

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 23;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 523 GCCTGCACCATGCAAG 539
DB 1 GCCUGCACCACCAAG 17
```



```
Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1381 AAGAGGAGGAGGAGG 1395
|||||
Db 1 AAGAGCAGGAGGAGG 15

RESULT 30
US-10-364-412A-5002
; Sequence 5002, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5002
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (24168)...(24182)
; OTHER INFORMATION: Chromosome = 6 Strand = positive ConnectionObjectNumber = 5100
US-10-364-412A-5002

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1292 CGATGAGGACGAGA 1306
|||||
Db 1 CGATGAGGATGAGA 15

RESULT 31
US-10-364-412A-5050
; Sequence 5050, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5050
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (589372)...(589386)
; OTHER INFORMATION: Chromosome = 7 Strand = negative ConnectionObjectNumber = 6170
US-10-364-412A-5050

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1292 CGATGAGGACGAGA 1306
|||||
Db 1 CGATGAGGATGAGA 15

RESULT 32
US-10-834-967-3378/c
; Sequence 3378, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connection Sequences for the Archaeoglobus fulgidus DSM 4304,
```

```
; TITLE OF INVENTION: complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 3378
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (1349931)...(1349946)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = neg CtronObjNum = 3378
US-10-834-967-3378

Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1381 AAGAGGAGGAGGAGG 1395
|||||
Db 16 AAGAGGAGGAGGAGG 2

RESULT 33
US-10-257-017B-145445/c
; Sequence 145445, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosir
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145445
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036625
US-10-257-017B-145445

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 CTCCTACCGAAAAA 261
|||||
Db 13 CTCCTACCGAAAAA 1

RESULT 34
US-10-257-017B-145446
; Sequence 145446, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosir
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145446
; LENGTH: 13
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036625
US-10-257-017B-145446

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 CTCACCGAAAAA 261
Db 1 CTCACCGAAAAA 13

RESULT 35
US-10-257-017B-151965/c
; Sequence 151965, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 151965
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038398
US-10-257-017B-151965

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAAA 1427
Db 13 CAACTTCAAAAAA 1

RESULT 36
US-10-257-017B-151966
; Sequence 151966, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 151966
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0038398
US-10-257-017B-151966

Query Match      0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1415 CAACTTCAAAAAA 1427
Db 1 CAACTTCAAAAAA 13

RESULT 37
US-10-708-951-20910
; Sequence 20910, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 20910
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-20910

Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 327 ATTAATTCCTGCG 339
Db 3 AUUAAAUUCUUGC 15

RESULT 38
US-10-708-951-46339
; Sequence 46339, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 46339
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-46339

Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 327 ATTAATTCCTGCG 339
Db 3 AUUAAAUUCUUGC 15

RESULT 39
US-10-708-951-21093/c
; Sequence 21093, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 21093
```

```
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-21093

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 463 TGGCAAGTGTCTGAA 478
Db 16 TTGTAAGTGTCTGAA 1

RESULT 40
US-10-708-951-46804/c
; Sequence 46804, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; FILE REFERENCE: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46804
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-46804

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 463 TGGCAAGTGTCTGAA 478
Db 16 TTGTAAGTGTCTGAA 1

RESULT 41
US-10-364-412A-5277
; Sequence 5277, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5277
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (235019)...(235035)
; OTHER INFORMATION: Chromosome = 6 Strand = positive ConnectronObjectNumber = 5427
US-10-364-412A-5277

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1294 ATGAGGACGAGACGA 1309
Db 1 ATGAGGACGAGACGA 16

RESULT 42
US-10-364-412A-7505
; Sequence 7505, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7505
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (1006862)...(1006877)
; OTHER INFORMATION: Chromosome = 12 Strand = negative ConnectronObjectNumber = 1071
US-10-364-412A-7505
```

```
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7505
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (768662)...(768678)
; OTHER INFORMATION: Chromosome = 15 Strand = positive ConnectronObjectNumber = 1361
US-10-364-412A-7505

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1294 ATGAGGACGAGACGA 1309
Db 1 ATGAGGACGAGACGA 16

RESULT 43
US-10-364-412A-7832/c
; Sequence 7832, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7832
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (999582)...(999597)
; OTHER INFORMATION: Chromosome = 12 Strand = negative ConnectronObjectNumber = 1071
US-10-364-412A-7832

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1294 ATGAGGACGAGACGA 1309
Db 16 ATGATGACGAGATGA 1

RESULT 44
US-10-364-412A-7834/c
; Sequence 7834, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 7834
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (1006862)...(1006877)
; OTHER INFORMATION: Chromosome = 12 Strand = negative ConnectronObjectNumber = 1071
US-10-364-412A-7834
```



```
US-10-364-412A-7834
Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1294 ATGAGGACGAAGACGA 1309
    |||||
Db 16 ATGATGACGAAGATGA 1

RESULT 45
US-10-364-412A-8999/c
; Sequence 8999, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 8999
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (768662)...(768678)
; OTHER INFORMATION: Chromosome =15 Strand = negative ConnectronObjectNumber = 13630
US-10-364-412A-8999

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1294 ATGAGGACGAAGACGA 1309
    |||||
Db 16 ATGACGACGACGACGA 1

RESULT 46
US-10-138-674B-5988
; Sequence 5988, Application US/10138674B
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5988
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674B-5988

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGCTGTGAAACT 481
    |||
Db 1 CAACUGCUUUGAAACU 16

RESULT 47
US-10-257-017B-41893
```

```
; Sequence 41893, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41893
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012555
US-10-257-017B-41893

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1004 GGGAGGCGGTGGT 1016
    |||||
Db 1 GGGAGGCGGTGGY 13

RESULT 48
US-10-257-017B-41894/c
; Sequence 41894, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41894
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012555
US-10-257-017B-41894

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1004 GGGAGGCGGTGGT 1016
    |||||
Db 13 GGGAGGCGGTGGY 1

RESULT 49
US-10-257-017B-48345
; Sequence 48345, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

```

; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 48345
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013790
US-10-257-017B-48345

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 853 TAATGGAGATGTT 865
DB 1 TAATGGAGATGTY 13

RESULT 50
US-10-257-017B-48346/c
; Sequence 48346, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 48346
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013790
US-10-257-017B-48346

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 853 TAATGGAGATGTT 865
DB 13 TAATGGAGATGTY 1

RESULT 51
US-10-257-017B-188275
; Sequence 188275, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 188275
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

```

; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046357
US-10-257-017B-188275

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 256 GAAAAATGGAAT 268
DB 1 GAAAAATGGAAY 13

RESULT 52
US-10-257-017B-188276/c
; Sequence 188276, Application US/10257017B
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 188276
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046357
US-10-257-017B-188276

Query Match      0.8%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 256 GAAAAATGGAAT 268
DB 13 GAAAAATGGAAY 1

RESULT 53
US-10-708-951-31160
; Sequence 31160, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31160
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-708-951-31160

Query Match      0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 269 CTATCGCCCTCACA 282
DB 1 CUAUCGCCAUCACA 14

RESULT 54
US-10-708-951-43411

```

```
; Sequence 43411, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43411
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-43411

Query Match      0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      269 CTATCGCCCTCACA 282
DB      1 CUAGCCCAUCACA 14

RESULT 55
US-10-796-280-67926/c
; Sequence 67926, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 67926
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-67926

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1268 GGACGCCATCCCTG 1281
DB      15 GGAAGCCATCCCTG 2

RESULT 56
US-10-708-951-20715
; Sequence 20715, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 20715
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-20715

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.8%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1559 AATGGACCTCTCCA 1572
DB      1 AAGGACCUCUCCA 14

RESULT 57
US-10-708-951-22787/c
; Sequence 22787, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 22787
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-22787

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      540 TTCACCATGCTGAC 653
DB      15 TTCACCATGCTGAC 2

RESULT 58
US-10-708-951-40578
; Sequence 40578, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 40578
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-40578

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1559 AATGGACCTCTCCA 1572
DB      1 AAGGACCUCUCCA 14

RESULT 59
US-10-708-951-45190/c
; Sequence 45190, Application US/10708951
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY BACTERIAL
; TITLE OF INVENTION: AND BACTERIAL ASSOCIATED OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 55034
; CURRENT APPLICATION NUMBER: US/10/708,951
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 59824
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 45190
```

```
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-708-951-45190

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 640 TTCACCATGTTGAC 653
   |||||
Db 15 TTCACCATGTTGAC 2

RESULT 60
US-10-834-967-1542
; Sequence 1542, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connection Sequences for the Archaeoglobus fulgidus DSM 4304,
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 1542
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (598308)...(598322)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = neg CtronObjNum = 1542
US-10-834-967-1542

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 876 GCGGTGGTCTTACA 889
   |||||
Db 2 GCGGTGGTCTTACA 15

RESULT 61
US-10-834-967-4433
; Sequence 4433, Application US/10834967
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.;
; TITLE OF INVENTION: Connection Sequences for the Archaeoglobus fulgidus DSM 4304,
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/834,967
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 5566
; SOFTWARE: Proprietary
; SEQ ID NO 4433
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Archaeoglobus fulgidus DSM 4304, complete genome.
; FEATURE:
; LOCATION: (1760153)...(1760167)
; OTHER INFORMATION: Chromosome = 1 Contig = 1 Strand = pos CtronObjNum = 4433
US-10-834-967-4433

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 876 GCGGTGGTCTTACA 889
   |||||
Db 2 GCGGTGGTCTTACA 15
```

```
RESULT 62
US-10-364-412A-1121/c
; Sequence 1121, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 1121
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (714110)...(714124)
; OTHER INFORMATION: Chromosome = 2 Strand = positive CtronObjNum = 13
US-10-364-412A-1121

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1293 GATGAGGACGAAGA 1306
   |||||
Db 14 GATGAGGACGAAGA 1

RESULT 63
US-10-364-412A-1178/c
; Sequence 1178, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 1178
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (720539)...(720553)
; OTHER INFORMATION: Chromosome = 7 Strand = negative CtronObjNum = 63
US-10-364-412A-1178

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1293 GATGAGGACGAAGA 1306
   |||||
Db 14 GATGAGGACGAAGA 1

RESULT 64
US-10-364-412A-3817/c
; Sequence 3817, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3817
; LENGTH: 15
; TYPE: DNA
```

```

; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (1118706)...(1118720)
; OTHER INFORMATION: Chromosome = 4 Strand = negative ConnectronObjectNumber = 3584
US-10-364-412A-3817

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1446 GAGGATGAAAAA 1459
    |||||
Db 14 GAGGATGAAGAAGA 1

RESULT 65
US-10-364-412A-3852/c
; Sequence 3852, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 3852
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (404987)...(404901)
; OTHER INFORMATION: Chromosome =13 Strand = positive ConnectronObjectNumber = 11539
US-10-364-412A-3852

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1446 GAGGATGAAAAA 1459
    |||||
Db 14 GAGGATGAAGAAGA 1

RESULT 66
US-10-364-412A-4291
; Sequence 4291, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 4291
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (274788)...(274802)
; OTHER INFORMATION: Chromosome = 5 Strand = positive ConnectronObjectNumber = 4481
US-10-364-412A-4291

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1444 CAGAGATGAAAAA 1457
    |||||
Db 1 CAGAGATGAAAAA 14
```

```

RESULT 67
US-10-364-412A-4292/c
; Sequence 4292, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 4292
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (274788)...(274802)
; OTHER INFORMATION: Chromosome = 5 Strand = negative ConnectronObjectNumber = 448
US-10-364-412A-4292

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1444 CAGAGATGAAAAA 1457
    |||||
Db 15 CAGAGATGAAAAA 2

RESULT 68
US-10-364-412A-5773/c
; Sequence 5773, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (720539)...(720553)
; OTHER INFORMATION: Chromosome = 7 Strand = negative ConnectronObjectNumber = 630
US-10-364-412A-5773

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1293 GATGAGGACGAAGA 1306
    |||||
Db 14 GATGAGGACGAAGA 1

RESULT 69
US-10-364-412A-5828/c
; Sequence 5828, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 5828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
```

```
; FEATURE:
; LOCATION: (251903)...(251919)
; OTHER INFORMATION: Chromosome =12 Strand = positive ConnectionObjectNumber = 9757
US-10-364-412A-5828
```

```
Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No.30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1293 CATGAGGACGAAGA 1306
Db 14 GATGAAGACGAAGA 1
```

RESULT 70

```
US-10-364-412A-6612
; Sequence 6612, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 6612
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (155118)...(155132)
; OTHER INFORMATION: Chromosome = 8 Strand = positive ConnectionObjectNumber = 7049
US-10-364-412A-6612
```

```
Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1412 TTCCAACCTTCAAAA 1425
Db 1 TTCCAACCTTCAAAA 14
```

RESULT 71

```
US-10-364-412A-6645
; Sequence 6645, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 6645
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (868980)...(868994)
; OTHER INFORMATION: Chromosome =16 Strand = negative ConnectionObjectNumber = 14895
US-10-364-412A-6645
```

```
Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No.30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1412 TTCCAACCTTCAAAA 1425
Db 1 TTCCAACCTTCAAAA 14
```

RESULT 72

```
US-10-364-412A-8313
; Sequence 8313, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 8313
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (58645)...(58659)
; OTHER INFORMATION: Chromosome =13 Strand = negative ConnectionObjectNumber = 1091
US-10-364-412A-8313
```

```
Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No.30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 568 TCAATGATATCGTC 581
Db 1 TCAATGATATCGAC 14
```

RESULT 73

```
US-10-364-412A-8326
; Sequence 8326, Application US/10364412A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Saccharomyces cerevisiae complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/364,412A
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 9208
; SOFTWARE: Proprietary
; SEQ ID NO 8326
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae complete genome.
; FEATURE:
; LOCATION: (195799)...(195813)
; OTHER INFORMATION: Chromosome =13 Strand = positive ConnectionObjectNumber = 111
US-10-364-412A-8326
```

```
Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No.30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 568 TCAATGATATCGTC 581
Db 1 TCAATGATATCGAC 14
```

Search completed: June 24, 2004, 10:25:54
Job time : 2 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:15:53 ; Search time 4 Seconds
(without alignments)
3.183 Million cell updates/sec

Title: US-09-817-538-2
Perfect score: 1611
Sequence: 1 atgtctgggtctctgcgcg.....tcctcagctttttttccc 1611

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 209 seqs, 3951 residues

Total number of hits satisfying chosen parameters: 418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 209 summaries

Database : rnpb2.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	26	1.6	26	1	US-09-563-728A-4
C 2	26	1.6	26	1	US-09-563-728A-13
C 3	26	1.6	26	1	US-10-145-493B-47
C 4	25.2	1.6	30	1	US-10-189-818B-39
C 5	25	1.6	26	1	US-10-145-493B-90
C 6	24.4	1.5	26	1	US-09-563-728A-2
C 7	24.4	1.5	26	1	US-09-563-728A-3
C 8	24.4	1.5	26	1	US-09-563-728A-11
C 9	24.4	1.5	26	1	US-09-563-728A-12
C 10	23.4	1.5	26	1	US-10-145-493B-82
C 11	23.4	1.5	26	1	US-10-145-493B-83
C 12	23	1.4	23	1	US-10-145-493B-45
C 13	22.8	1.4	26	1	US-09-563-728A-14
C 14	22.8	1.4	26	1	US-09-563-728A-5
C 15	22.8	1.4	26	1	US-10-145-493B-55
C 16	22	1.4	22	1	US-10-145-493B-46
C 17	21.8	1.4	26	1	US-10-145-493B-89
C 18	21.4	1.3	22	1	US-10-145-493B-53
C 19	20.4	1.3	22	1	US-10-145-493B-54
C 20	20	1.2	20	1	US-09-754-167-12
C 21	20	1.2	20	1	US-09-754-167-13
C 22	20	1.2	20	1	US-09-754-167-14
C 23	20	1.2	20	1	US-09-754-167-15
C 24	20	1.2	20	1	US-09-754-167-16
C 25	20	1.2	20	1	US-09-754-167-17
C 26	20	1.2	20	1	US-09-754-167-18
C 27	20	1.2	20	1	US-09-754-167-19
C 28	20	1.2	20	1	US-09-754-167-20
C 29	20	1.2	20	1	US-09-754-167-21
C 30	20	1.2	20	1	US-09-754-167-22
C 31	20	1.2	20	1	US-09-754-167-23
C 32	20	1.2	20	1	US-09-754-167-24
C 33	20	1.2	20	1	US-09-754-167-25

Sequence 26, Appl	1	US-09-754-167-26	20	1.2	20	C 34
Sequence 27, Appl	1	US-09-754-167-27	20	1.2	20	C 35
Sequence 29, Appl	1	US-09-754-167-29	20	1.2	20	C 36
Sequence 30, Appl	1	US-09-754-167-30	20	1.2	20	C 37
Sequence 31, Appl	1	US-09-754-167-31	20	1.2	20	C 38
Sequence 32, Appl	1	US-09-754-167-32	20	1.2	20	C 39
Sequence 33, Appl	1	US-09-754-167-33	20	1.2	20	C 40
Sequence 34, Appl	1	US-09-754-167-34	20	1.2	20	C 41
Sequence 35, Appl	1	US-09-754-167-35	20	1.2	20	C 42
Sequence 36, Appl	1	US-09-754-167-36	20	1.2	20	C 43
Sequence 37, Appl	1	US-09-754-167-37	20	1.2	20	C 44
Sequence 38, Appl	1	US-09-754-167-38	20	1.2	20	C 45
Sequence 39, Appl	1	US-09-754-167-39	20	1.2	20	C 46
Sequence 40, Appl	1	US-09-754-167-40	20	1.2	20	C 47
Sequence 41, Appl	1	US-09-754-167-41	20	1.2	20	C 48
Sequence 42, Appl	1	US-09-754-167-42	20	1.2	20	C 49
Sequence 43, Appl	1	US-09-754-167-43	20	1.2	20	C 50
Sequence 44, Appl	1	US-09-754-167-44	20	1.2	20	C 51
Sequence 45, Appl	1	US-09-754-167-45	20	1.2	20	C 52
Sequence 46, Appl	1	US-09-754-167-46	20	1.2	20	C 53
Sequence 47, Appl	1	US-09-754-167-47	20	1.2	20	C 54
Sequence 48, Appl	1	US-09-754-167-48	20	1.2	20	C 55
Sequence 49, Appl	1	US-09-754-167-49	20	1.2	20	C 56
Sequence 50, Appl	1	US-09-754-167-50	20	1.2	20	C 57
Sequence 51, Appl	1	US-09-754-167-51	20	1.2	20	C 58
Sequence 52, Appl	1	US-09-754-167-52	20	1.2	20	C 59
Sequence 54, Appl	1	US-09-754-167-54	20	1.2	20	C 60
Sequence 55, Appl	1	US-09-754-167-55	20	1.2	20	C 61
Sequence 56, Appl	1	US-09-754-167-56	20	1.2	20	C 62
Sequence 57, Appl	1	US-09-754-167-57	20	1.2	20	C 63
Sequence 58, Appl	1	US-09-754-167-58	20	1.2	20	C 64
Sequence 59, Appl	1	US-09-754-167-59	20	1.2	20	C 65
Sequence 60, Appl	1	US-09-754-167-60	20	1.2	20	C 66
Sequence 61, Appl	1	US-09-754-167-61	20	1.2	20	C 67
Sequence 62, Appl	1	US-09-754-167-62	20	1.2	20	C 68
Sequence 63, Appl	1	US-09-754-167-63	20	1.2	20	C 69
Sequence 64, Appl	1	US-09-754-167-64	20	1.2	20	C 70
Sequence 17, Appl	1	US-09-817-913-17	20	1.2	20	C 71
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 72
Sequence 17, Appl	1	US-09-817-913-17	20	1.2	20	C 73
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 74
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 75
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 76
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 77
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 78
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 79
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 80
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 81
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 82
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 83
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 84
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 85
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 86
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 87
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 88
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 89
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 90
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 91
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 92
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 93
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 94
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 95
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 96
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 97
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 98
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 99
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 100
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 101
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 102
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 103
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 104
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 105
Sequence 18, Appl	1	US-09-817-913-18	20	1.2	20	C 106

```
107 14.8 0.9 18 1 US-09-923-246-23 Sequence 23, Appl
108 14.8 0.9 18 1 US-10-285-723-23 Sequence 23, Appl
109 14.8 0.9 18 1 US-10-243-072-22 Sequence 39, Appl
110 14.8 0.9 18 1 US-10-243-072-22 Sequence 39, Appl
111 14.8 0.9 18 1 US-10-414-186-22 Sequence 22, Appl
112 14.8 0.9 18 1 US-10-414-186-22 Sequence 22, Appl
113 14.8 0.9 18 1 US-10-414-186-22 Sequence 22, Appl
114 14.8 0.9 18 1 US-10-659-684-23 Sequence 23, Appl
115 14.4 0.9 16 1 US-09-935-868-3 Sequence 3, Appl
116 14.4 0.9 16 1 US-10-287-035-3 Sequence 3, Appl
117 14.4 0.9 16 1 US-10-282-162-3 Sequence 3, Appl
118 14.4 0.9 16 1 US-10-138-674-5827 Sequence 5827, Ap
119 14.4 0.9 17 1 US-09-866-108-971 Sequence 971, App
120 14.4 0.9 17 1 US-09-866-108-972 Sequence 972, App
121 14.4 0.9 17 1 US-09-866-108-972 Sequence 972, App
122 14.4 0.9 17 1 US-09-780-164-387 Sequence 387, App
123 14.4 0.9 17 1 US-09-780-164-387 Sequence 387, App
124 14.4 0.9 17 1 US-09-780-164-387 Sequence 387, App
125 14.4 0.9 17 1 US-10-138-674-4754 Sequence 4754, Ap
126 14.4 0.9 17 1 US-10-287-949A-4754 Sequence 4754, Ap
127 14.4 0.9 18 1 US-09-861-779-4 Sequence 4, Appl
128 14.4 0.9 18 1 US-10-636-716-4 Sequence 46, Appl
129 14.4 0.9 18 1 US-10-269-557-46 Sequence 165, App
130 14.4 0.9 18 1 US-10-387-438-165 Sequence 4102, Ap
131 14.4 0.9 18 1 US-10-349-143-4102 Sequence 5179, Ap
132 14.4 0.9 18 1 US-10-349-143-9179 Sequence 6562, Ap
133 13.8 0.9 17 1 US-09-866-108-6562 Sequence 7084, Ap
134 13.8 0.9 17 1 US-09-866-108-7084 Sequence 8667, Ap
135 13.8 0.9 17 1 US-09-866-108-8667 Sequence 8668, Ap
136 13.8 0.9 17 1 US-09-866-108-8668 Sequence 117, App
137 13.8 0.9 17 1 US-09-961-077-117 Sequence 66, Appl
138 13.8 0.9 17 1 US-09-784-674-66 Sequence 438, App
139 13.8 0.9 17 1 US-09-877-478-438 Sequence 3128, Ap
140 13.8 0.9 17 1 US-09-848-754A-3128 Sequence 723, App
141 13.8 0.9 17 1 US-09-827-395A-723 Sequence 1709, Ap
142 13.8 0.9 17 1 US-09-740-332-1709 Sequence 1724, Ap
143 13.8 0.9 17 1 US-09-740-332-1724 Sequence 2831, Ap
144 13.8 0.9 17 1 US-09-740-332-2831 Sequence 2846, Ap
145 13.8 0.9 17 1 US-09-740-332-2846 Sequence 4133, Ap
146 13.8 0.9 17 1 US-09-740-332-4133 Sequence 95, Appl
147 13.8 0.9 17 1 US-09-792-818-95 Sequence 1709, Ap
148 13.8 0.9 17 1 US-09-817-879-1709 Sequence 1724, Ap
149 13.8 0.9 17 1 US-09-817-879-1724 Sequence 2831, Ap
150 13.8 0.9 17 1 US-09-817-879-2831 Sequence 2846, Ap
151 13.8 0.9 17 1 US-09-817-879-2846 Sequence 4133, Ap
152 13.8 0.9 17 1 US-09-817-879-4133 Sequence 438, App
153 13.8 0.9 17 1 US-10-342-902-438 Sequence 108, App
154 13.8 0.9 17 1 US-09-949-238-2 Sequence 723, App
155 13.8 0.9 17 1 US-09-927-046-108 Sequence 756A-591
156 13.8 0.9 17 1 US-10-430-882-723 Sequence 589, App
157 13.8 0.9 17 1 US-10-060-756A-588 Sequence 590, App
158 13.8 0.9 17 1 US-10-060-756A-590 Sequence 591, App
159 13.8 0.9 17 1 US-10-060-756A-591 Sequence 1329, Ap
160 13.8 0.9 17 1 US-10-060-998-1329 Sequence 559, App
161 13.8 0.9 17 1 US-10-163-552-559 Sequence 4432, Ap
162 13.8 0.9 17 1 US-10-155-306-4432 Sequence 4966, Ap
163 13.8 0.9 17 1 US-10-155-306-4966 Sequence 5328, Ap
164 13.8 0.9 17 1 US-10-155-306-5328 Sequence 6388, Ap
165 13.8 0.9 17 1 US-10-155-306-6388 Sequence 3037, Ap
166 13.8 0.9 17 1 US-10-238-700-3037 Sequence 3128, Ap
167 13.8 0.9 17 1 US-10-238-700-3128 Sequence 240, App
168 13.8 0.9 17 1 US-10-339-782-240 Sequence 971, App
169 13.8 0.9 17 1 US-10-297-068-971 Sequence 947, App
170 13.8 0.9 17 1 US-10-138-674-947 Sequence 2635, Ap
171 13.8 0.9 17 1 US-10-138-674-2635 Sequence 4755, Ap
172 13.8 0.9 17 1 US-10-138-674-4755 Sequence 4756, Ap
173 13.8 0.9 17 1 US-10-138-674-4756 Sequence 4757, Ap
174 13.8 0.9 17 1 US-10-138-674-4757 Sequence 4758, Ap
175 13.8 0.9 17 1 US-10-138-674-4758 Sequence 5394, Ap
176 13.8 0.9 17 1 US-10-138-674-5394 Sequence 7633, Ap
177 13.8 0.9 17 1 US-10-138-674-7633 Sequence 947, App
178 13.8 0.9 17 1 US-10-287-949A-947 Sequence 2635, Ap
179 13.8 0.9 17 1 US-10-287-949A-947 Sequence 4755, Ap
180 13.8 0.9 17 1 US-10-287-949A-4755 Sequence 4756, Ap
181 13.8 0.9 17 1 US-10-287-949A-4756 Sequence 4757, Ap
182 13.8 0.9 17 1 US-10-287-949A-4757 Sequence 4758, Ap
183 13.8 0.9 17 1 US-10-287-949A-4758 Sequence 5394, Ap
184 13.8 0.9 17 1 US-10-287-949A-5394 Sequence 7633, Ap
185 13.8 0.9 17 1 US-10-287-949A-7633 Sequence 978, App
186 13.8 0.9 17 1 US-10-712-672-978 Sequence 2255, Ap
187 13.8 0.9 17 1 US-10-712-672-2255 Sequence 1912, Ap
188 13.8 0.9 17 1 US-10-712-672-1912 Sequence 1925, Ap
189 13.4 0.8 15 1 US-10-287-919-1925 Sequence 19, Appl
190 13.4 0.8 15 1 US-09-420-433-19 Sequence 18, Appl
191 13.4 0.8 15 1 US-09-420-433-19 Sequence 253, App
192 13 0.8 15 1 US-10-056-414-258 Sequence 250, App
193 13 0.8 15 1 US-10-056-414-258 Sequence 48, Appl
194 13 0.8 15 1 US-10-043-875-350 Sequence 3505, Ap
195 13 0.8 15 1 US-10-101-030B-48 Sequence 3483, Ap
196 13 0.8 15 1 US-10-084-839-3505 Sequence 3501, Ap
197 13 0.8 16 1 US-10-084-839-3483 Sequence 330, App
198 13 0.8 16 1 US-10-126-022-330 Sequence 124, App
199 13 0.8 16 1 US-10-126-022-330 Sequence 124, App
200 13 0.8 16 1 US-08-591-486B-124 Sequence 11, Appl
201 12.8 0.8 16 1 US-09-739-928-11 Sequence 569, App
202 12.8 0.8 16 1 US-10-339-674-569 Sequence 22, Appl
203 12.8 0.8 16 1 US-10-059-888-22 Sequence 22, Appl
204 12.8 0.8 16 1 US-10-059-877-22 Sequence 35, Appl
205 12.8 0.8 16 1 US-10-065-133A-35 Sequence 35, Appl
206 12.8 0.8 16 1 US-10-434-811A-35 Sequence 5988, Ap
207 12.8 0.8 16 1 US-10-138-674-5988 Sequence 5988, Ap
208 12.8 0.8 16 1 US-10-138-674-5988 Sequence 5988, Ap
209 12.8 0.8 16 1 US-10-287-949A-5988 Sequence 5988, Ap

ALIGNMENTS

RESULT 1
US-09-563-728A-4/c
; Sequence 4, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: Macleod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09563728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-4

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATATTTGCTG 236
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 26 GAATCCGCATGACTCATATTTGCTG 1

RESULT 2
US-09-563-728A-13/c
; Sequence 13, Application US/09563728A
; Publication No. US20030078216A1
```


GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-13

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATATAATTGCTG 236
DB 26 GAATCCGCATGACTCATATAATTGCTG 1

RESULT 3
US-10-145-493B-47/c
; Sequence 47, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-01SDV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-47

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATATAATTGCTG 236
DB 26 GAATCCGCATGACTCATATAATTGCTG 1

RESULT 4
US-10-189-818B-39/c
; Sequence 39, Application US/10189818B
; Publication No. US20040072770A1
; GENERAL INFORMATION:

; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELOREME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-189-818B-39

Query Match 1.6%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 8.5;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1533 GTCAGGAGGAGGCGCAAGTTGGCTGAATG 1562
DB 30 GTCAGGAGGAGGCGCAAGTTGGCTGAATG 1

RESULT 5
US-10-145-493B-90/c
; Sequence 90, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-01SDV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-90

Query Match 1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATATAATTGCTG 236
DB 25 AATCCGCATGACTCATATAATTGCTG 1

RESULT 6
US-09-563-728A-2/c
; Sequence 2, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A

```

; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-2

Query Match          1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 8;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      211 GAATCCGCATGACTCATAAATTGCTG 236
        |||||
Db      26 GAATCCGCATGACCCATAAATTGCTG 1

RESULT 7
US-09-563-728A-3/c
; Sequence 3, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 3
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-3

Query Match          1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 8;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      211 GAATCCGCATGACTCATAAATTGCTG 236
        |||||
Db      26 GAATCCGCATGACCCATAAATTGCTG 1

RESULT 8
US-09-563-728A-11/c
; Sequence 11, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-11

Query Match          1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 8;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      211 GAATCCGCATGACTCATAAATTGCTG 236
        |||||
Db      26 GAATCCGCATGACCCATAAATTGCTG 1

RESULT 9
US-09-563-728A-12/c
; Sequence 12, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-12

Query Match          1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 8;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      211 GAATCCGCATGACTCATAAATTGCTG 236
        |||||
Db      26 GAATCCGCATGACCCATAAATTGCTG 1

RESULT 10
US-10-145-493B-82/c
; Sequence 82, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 82
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-10-145-493B-82/c

```

```
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-82

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGATGACTCATAAATTGCTG 236
Db 25 AATCCGATGACCCATAAATTGCTG 1

RESULT 11
US-10-145-493B-83/c
; Sequence 83, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 83
; SOFTWARE: PatentIn version 3.0
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-83

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGATGACTCATAAATTGCTG 236
Db 25 AATCCGATGACCCATAAATTGCTG 1

RESULT 12
US-10-145-493B-45/c
; Sequence 45, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 45
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-45

Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCGTGTACTACTACGACGG 160
Db 23 AAAGTCGTGTACTACTACGACGG 1

RESULT 13
US-09-563-728A-5/c
; Sequence 5, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-563-728A-5

Query Match      1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGATGACTCATAAATTGCTG 236
Db 26 GAATCCGATGACCCATAAATTGCTG 1

RESULT 14
US-09-563-728A-14/c
; Sequence 14, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
```

; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
US-09-563-728A-14

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
DB 26 GAATCCGCATGACCCATAACTTGCTG 1

RESULT 15

US-10-145-493B-55/c

; Sequence 55, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 55

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-55

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
DB 26 GAATCCGCATGACCCATAACTTGCTG 1

RESULT 16

US-10-145-493B-46/c

; Sequence 46, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 46

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer
US-10-145-493B-46

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAATTAATTAATGACA 187
DB 22 TTGGAATTAATTAATGACA 1

RESULT 17

US-10-145-493B-89/c

; Sequence 89, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 89

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-89

Query Match 1.4%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 19;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236
DB 25 AATCCGCATGACCCATAACTTGCTG 1

RESULT 18

US-10-145-493B-53/c

; Sequence 53, Application US/10145493B

; Publication No. US20030096777A1

; GENERAL INFORMATION:

; APPLICANT: Besterman, Jeffrey

; APPLICANT: MacLeod, Robert

; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

; FILE REFERENCE: MET-015DV

; CURRENT APPLICATION NUMBER: US/10/145,493B

; CURRENT FILING DATE: 2002-05-14

; PRIOR APPLICATION NUMBER: 09/420,692

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: US 60/104,804

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 53

; LENGTH: 23

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-10-145-493B-53

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 16;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAGTCTGTTACTACTAGCG 160
DB 23 AAGTCTGTTACTACTAGCG 1

RESULT 19
US-10-145-493B-54/c
; Sequence 54, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-54

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAAATTACTATTATGACA 187
DB 22 TTGGAAATTACTATTATGACA 1

RESULT 20
US-09-754-167-12/c
; Sequence 12, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-12

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCGGACAGATGCGCGAGA 120
DB 20 GCGGACAGATGCGCGAGA 1

RESULT 21
US-09-754-167-13/c
; Sequence 13, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-13

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GAGAAAGTCTGTACTACT 153
DB 20 GAGAAAGTCTGTACTACT 1

RESULT 22
US-09-754-167-14/c
; Sequence 14, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-14

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 AATTGCTGCTCAACTATGG 247
DB 20 AATTGCTGCTCAACTATGG 1

RESULT 23
US-09-754-167-15/c
; Sequence 15, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-15

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 GCTGCTCAACTATGGTCTCT 252
      |||||
Db 20 GCTGCTCAACTATGGTCTCT 1

RESULT 24
US-09-754-167-16/c
; Sequence 16, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-16

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TCAACTATGGTCTCTACCGA 257
      |||||
Db 20 TCAACTATGGTCTCTACCGA 1

RESULT 25
US-09-754-167-17/c
; Sequence 17, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-17

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATGCTCTCTACCGAANAAT 262
      |||||
Db 20 TATGCTCTCTACCGAANAAT 1

RESULT 26
US-09-754-167-18/c
; Sequence 18, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-18

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CGCCCTCACAAGGCAATGC 292
      |||||
Db 20 CGCCCTCACAAGGCAATGC 1

RESULT 27
US-09-754-167-19/c
; Sequence 19, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-19

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCAATGCTGAGG 297
      |||||
Db 20 TCACAAAGCCAATGCTGAGG 1

RESULT 28
US-09-754-167-20/c
; Sequence 20, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-20

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 AAGCCAAATGCTGAGGAGATG 302
      |||||
DB 20 AAGCCAAATGCTGAGGAGATG 1

RESULT 29
US-09-754-167-21/c
; Sequence 21, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-21

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 AATGCTGAGGAGATGACCAA 307
      |||||
DB 20 AATGCTGAGGAGATGACCAA 1

RESULT 30
US-09-754-167-22/c
; Sequence 22, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-22

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 TGAGGAGATGACCAAGTACC 312
      |||||
DB 20 TGAGGAGATGACCAAGTACC 1

RESULT 31
US-09-754-167-23/c
; Sequence 23, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-23

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TACAGCAAGCAGATGCGAG 388
      |||||
DB 20 TACAGCAAGCAGATGCGAG 1

RESULT 32
US-09-754-167-24/c
; Sequence 24, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-24

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 GACTGTCCAGTATTCGATGG 424
      |||||
DB 20 GACTGTCCAGTATTCGATGG 1

RESULT 33
US-09-754-167-25/c
; Sequence 25, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-25

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 TGTTGAGTCTCTCAGTTG 446
    |||||
Db 20 TGTTGAGTCTCTCAGTTG 1

RESULT 34
US-09-754-167-26/c
; Sequence 26, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-26

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 CTTAATAAGCAGCAGACGGA 499
    |||||
Db 20 CTTAATAAGCAGCAGACGGA 1

RESULT 35
US-09-754-167-27/c
; Sequence 27, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-27

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 TAAGCAGCAGCAGACATCG 504
    |||||
Db 20 TAAGCAGCAGCAGACATCG 1

RESULT 36
US-09-754-167-29/c
; Sequence 29, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-29

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 ATCGTCTGGCCATCCTGGA 595
    |||||
Db 20 ATCGTCTGGCCATCCTGGA 1

RESULT 37
US-09-754-167-30/c
; Sequence 30, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-30

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 CTTGCCCATCCTGGAATGC 600
    |||||
Db 20 CTTGCCCATCCTGGAATGC 1

RESULT 38
US-09-754-167-31/c
; Sequence 31, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-31
```



```
US-09-754-167-31
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GCGGTGGAGAGCGCTTCTA 573
Db 20 GCGGTGGAGAGCGCTTCTA 1

RESULT 39
US-09-754-167-32/c
; Sequence 32, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-32

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 GAGGCGTCTTACACCAACGGA 582
Db 20 GAGGCGTCTTACACCAACGGA 1

RESULT 40
US-09-754-167-33/c
; Sequence 33, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-33

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 GGAGAGTACTTCCAGGAAC 733
Db 20 GGAGAGTACTTCCAGGAAC 1

RESULT 41
US-09-754-167-34/c
; Sequence 34, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-34

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTTCCAGGAAGCTGGG 738
Db 20 GTACTTCCAGGAAGCTGGG 1

RESULT 42
US-09-754-167-35/c
; Sequence 35, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-35

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 TCCAGGAAGCTGGGACCTA 743
Db 20 TCCAGGAAGCTGGGACCTA 1

RESULT 43
US-09-754-167-36/c
; Sequence 36, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-36
```

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 GGAACGGGACCTACGGGA 748
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GGAACGGGACCTACGGGA 1

RESULT 44
US-09-754-167-37/c
; Sequence 37, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-37

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 AGTATTATGCTGTTAACTAC 788
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AGTATTATGCTGTTAACTAC 1

RESULT 45
US-09-754-167-38/c
; Sequence 38, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-38

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 CCCGCTCCGACGGGATTG 807
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCCGCTCCGACGGGATTG 1

RESULT 46
US-09-754-167-39/c
; Sequence 39, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-39

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACGAGTCCTATGAGGCCATT 830
| | | | | | | | | | | | | | | | | | | | | |
Db 20 ACGAGTCCTATGAGGCCATT 1

RESULT 47
US-09-754-167-40/c
; Sequence 40, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-40

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GTCATGTCCAAAGTAATGGA 859
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GTCATGTCCAAAGTAATGGA 1

RESULT 48
US-09-754-167-41/c
; Sequence 41, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-41

```
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 845 GTCCAAAGTAATGGAGATCT 864
Db 20 GTCCAAAGTAATGGAGATCT 1

RESULT 49
US-09-754-167-42/c
; Sequence 42, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RFS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 42:
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-42

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 AAGTAATGGAGATGTTCCAG 869
Db 20 AAGTAATGGAGATGTTCCAG 1

RESULT 50
US-09-754-167-43/c
; Sequence 43, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RFS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 43:
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-43

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 AGATGTTCCAGCTAGTGGC 878
Db 20 AGATGTTCCAGCTAGTGGC 1

RESULT 51
US-09-754-167-44/c
; Sequence 44, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
```

```
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RFS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 44:
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-44

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 905 CCTATCTGGGATCGGTTAG 924
Db 20 CCTATCTGGGATCGGTTAG 1

RESULT 52
US-09-754-167-45/c
; Sequence 45, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RFS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 45:
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-45

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 CGGTTAGTTCCTTCAATCT 937
Db 20 CGGTTAGTTCCTTCAATCT 1

RESULT 53
US-09-754-167-46/c
; Sequence 46, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RFS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 46:
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-46

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 CGGTTAGTTCCTTCAATCT 937
Db 20 CGGTTAGTTCCTTCAATCT 1
```

Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 942 ATCAAGGACACGCCAAGTG 961
 |||||
 Db 20 ATCAAGGACACGCCAAGTG 1

RESULT 54
 US-09-754-167-47/c
 ; Sequence 47, Application US/09754167
 ; Patent No. US20010019328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
 ; FILE REFERENCE: RTS-0140
 ; CURRENT APPLICATION NUMBER: US/09/754,167
 ; CURRENT FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 47
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-754-167-47

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 947 AGGACAGCCCAAGTGTTGG 966
 |||||
 Db 20 AGGACAGCCCAAGTGTTGG 1

RESULT 55
 US-09-754-167-48/c
 ; Sequence 48, Application US/09754167
 ; Patent No. US20010019328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
 ; FILE REFERENCE: RTS-0140
 ; CURRENT APPLICATION NUMBER: US/09/754,167
 ; CURRENT FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 48
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-754-167-48

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1006 GAGCGGTGGTTACACCAT 1025
 |||||
 Db 20 GAGCGGTGGTTACACCAT 1

RESULT 56
 US-09-754-167-49/c
 ; Sequence 49, Application US/09754167
 ; Patent No. US20010019328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
 ; FILE REFERENCE: RTS-0140
 ; CURRENT APPLICATION NUMBER: US/09/754,167
 ; CURRENT FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 49
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-754-167-49

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1056 ACAGCTGGCCCTGGATAC 1075
 |||||
 Db 20 ACAGCTGGCCCTGGATAC 1

RESULT 57
 US-09-754-167-50/c
 ; Sequence 50, Application US/09754167
 ; Patent No. US20010019328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
 ; FILE REFERENCE: RTS-0140
 ; CURRENT APPLICATION NUMBER: US/09/754,167
 ; CURRENT FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 50
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-754-167-50

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 19; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1099 ACAATGACTACTTGAATAC 1118
 |||||
 Db 20 ACAATGACTACTTGAATAC 1

RESULT 58
 US-09-754-167-51/c
 ; Sequence 51, Application US/09754167
 ; Patent No. US20010019328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
 ; FILE REFERENCE: RTS-0140
 ; CURRENT APPLICATION NUMBER: US/09/754,167
 ; CURRENT FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 87
 ; SEQ ID NO 51
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-754-167-51

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 19;

```

; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-55

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 GACCTGTACAAGCGCATCTC 1327
      |||||
Db 20 GACCTGTACAAGCGCATCTC 1

RESULT 62
US-09-754-167-56/c
; Sequence 56, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-56

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCCTGTGAGGAAGAGT 1369
      |||||
Db 20 ATTGCCTGTGAGGAAGAGT 1

RESULT 63
US-09-754-167-57/c
; Sequence 57, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-57

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1378 CTCAGAGGAGGAGGAGG 1397
|||||
Db 20 CTCAGAGGAGGAGGAGG 1

RESULT 64

US-09-754-167-58/c
; Sequence 58, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 58
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-58

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATGAAAAGAGAAAGACCC 1468
|||||
Db 20 GATGAAAAGAGAAAGACCC 1

RESULT 65

US-09-754-167-59/c
; Sequence 59, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 59
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-59

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GAAACCAAGAGAGAGGC 1518
|||||
Db 20 GAAACCAAGAGAGAGGC 1

RESULT 66

US-09-754-167-60/c
; Sequence 60, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140

; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-60

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
|||||
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 67

US-09-754-167-61/c
; Sequence 61, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 61
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-61

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 GAGGAGAGCCAGAGCCAA 1528
|||||
Db 20 GAGGAGAGCCAGAGCCAA 1

RESULT 68

US-09-754-167-62/c
; Sequence 62, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 62
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-62

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1514 GAAGCCAGAGCCAAAGGGG 1533
Db 20 GAAGCCAGAGCCAAAGGGG 1

RESULT 69
US-09-754-167-63/c
; Sequence 63, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-63

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAGTTGCCCTGAATGACCT 1567
Db 20 AAGTTGCCCTGAATGACCT 1

RESULT 70
US-09-754-167-64/c
; Sequence 64, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-64

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 71
US-09-817-913-17/c
; Sequence 17, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 72
US-09-817-913-18/c
; Sequence 18, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-913-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 73
US-09-817-538-17/c
; Sequence 17, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
```

US-09-817-538-17

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604

DB 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 74

US-09-817-538-18/c
; Sequence 18, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
; FILE OF INVENTION: Deacetylase Isoforms
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-817-538-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584

DB 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 75

US-09-563-728A-1/c
; Sequence 1, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-563-728A-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604

DB 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 76
US-09-563-728A-10/c
; Sequence 10, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 17-20 are modified
; OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-16 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-10

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604

DB 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 77

US-10-189-818B-8/c
; Sequence 8, Application US/10189818B
; Publication No. US20040072770A1
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-189-818B-8

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604

Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 78

US-10-145-493B-35/c
; Sequence 35, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFELS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACETYLASE-7 AND 8
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-145-493B-35

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1565 CCTCTCCAGCTCTGGCTTCC 1584

Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 79

US-10-145-493B-35/c
; Sequence 35, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY
; APPLICANT: MACLEOD, ROBERT
; APPLICANT: SIDERS, WILLIAM
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-35

Query Match

Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 CCGCTGGTGGTCTCTCTC 36

Db 20 CCGCTGGTGGTCTCTCTC 1

RESULT 80

US-10-145-493B-36/c
; Sequence 36, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY
; APPLICANT: MACLEOD, ROBERT
; APPLICANT: SIDERS, WILLIAM
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-36

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 GCTGTCTCCCACTCGGTTCAT 48

Db 20 GCTGTCTCCCACTCGGTTCAT 1

RESULT 81

US-10-145-493B-37/c
; Sequence 37, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY
; APPLICANT: MACLEOD, ROBERT
; APPLICANT: SIDERS, WILLIAM
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-37

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 TGTCTCCCACTCGGTTCATCC 50

Db 20 TGTCTCCCACTCGGTTCATCC 1

RESULT 82

```
US-10-145-493B-38/c
; Sequence 38, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-38

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTATCTCTG 52
Db 20 TCTCCCACTCGGTATCTCTG 1

RESULT 83
US-10-145-493B-39/c
; Sequence 39, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTATCTCTGAGACACA 60
Db 20 TCGGTATCTCTGAGACACA 1

RESULT 84
US-10-145-493B-41/c
; Sequence 41, Application US/10145493B
; Publication No. US2003009677A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 85
US-10-145-493B-43/c
; Sequence 43, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-43

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 86
US-10-145-493B-44/c
; Sequence 44, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
```

; APPLICANT: Sigers, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-44

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 87

US-10-052-390B-1/c
; Sequence 1, Application US/10052390B
; Publication No. US20030148970A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 88

US-10-052-390B-2/c
; Sequence 2, Application US/10052390B
; Publication No. US20030148970A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.

; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-2

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
|||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 89

US-10-051-819B-1/c
; Sequence 1, Application US/10051819B
; Publication No. US20030152557A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCACGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 90

US-10-051-819B-2/c
; Sequence 2, Application US/10051819B
; Publication No. US20030152557A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon
; APPLICANT: Vaisburg, Arkadii

```

; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Ricc
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-2

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 91
US-09-733-692A-24/c
; Sequence 24, Application US/09733692A
; Patent No. US2002015581A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIV) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HPIV1 HN
US-09-733-692A-24

Query Match      1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 633 ATTGATTTCACCATGTCAGCGC 656
Db 24 ATTGCTATTTCACCATGTCAGCGC 1

RESULT 92
US-09-754-167-28/c
; Sequence 28, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-28

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 490 AGCAGACGGACATCGCGTG 509
Db 20 AGCAGACGGACATCGCGTG 1

RESULT 93
US-09-754-167-53/c
; Sequence 53, Application US/09754167
; Patent No. US20010019328A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-53

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1246 TCCAAACGCGAGCGGATTCCT 1265
Db 20 TCCAAATGCGAGCGGATTCCT 1

RESULT 94
US-10-145-493B-40/c
; Sequence 40, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-145-493B-40/c
```

```
; OTHER INFORMATION: primer
US-10-145-493B-40

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 62 CTTGAGCGCTCTGTCACTC 81
DB 20 CTTGAGCGCTCTGTCACTC 1

RESULT 95
US-10-145-493B-42/c
; Sequence 42, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-42

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1531 GGGTCAAGGAGAGGCCAAG 1550
DB 20 GGGTCAAGGAGAGGCCAAG 1

RESULT 96
US-09-953-318-65/c
; Sequence 65, Application US/09953318
; Publication No. US2003010536A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/09/953,318
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-318-65

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGCGCTGCACCATGCAA 537
```

```
DB 20 TGGGAGCGCTGCACCAAGCAA 1

RESULT 97
US-10-446-373-65/c
; Sequence 65, Application US/10446373
; Publication No. US20030204076A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/10/446,373
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/953,318
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-446-373-65

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGCGCTGCACCATGCAA 537
DB 20 TGGGAGCGCTGCACCAAGCAA 1

RESULT 98
US-09-995-529-198/c
; Sequence 198, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-995-529-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 40;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCCA 1469
DB 17 AAAAAGAGAAAGAYCCA 1

RESULT 99
US-09-995-529-198/c
; Sequence 198, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
```

```
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-995-529-198

Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 40;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1453 AAAAGAGAGAGACCCA 1469
Db 17 AAAAGAGAGAGAYCCA 1

RESULT 100
US-09-996-263-13/c
; Sequence 13, Application US/09996263
; Publication No. US20030004325A1
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1Iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,263
; FILING DATE: 28-Nov-02 US20030004325A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-996-263-13

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 40;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 101
US-10-057-550-28/c
; Sequence 28, Application US/10057550
; Publication No. US20030032607A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-28

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 102
US-10-173-225B-27/c
; Sequence 27, Application US/10173225B
; Publication No. US20030119769A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0665
; CURRENT APPLICATION NUMBER: US/10/173,225B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 10/057,550
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
```



```
Db      17 AGAGGAGAGAGATGGAA 1
|||||
RESULT 107
US-09-923-246-23
; Sequence 23, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-923-246-23
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCGCTGC 528
      |||||||
Db      1 ACTGGGCTGGGGGACTGC 18

RESULT 108
US-10-295-723-23
; Sequence 23, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCGCTGC 528
      |||||||
Db      1 ACTGGGCTGGGGGACTGC 18

RESULT 109
US-10-243-072-22
; Sequence 22, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-22
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCGCTGC 528
      |||||||
Db      1 ACTGGGCTGGGGGACTGC 18

RESULT 110
US-10-243-072-39
; Sequence 39, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
```



```
FILE REFERENCE: 98-55C1
CURRENT APPLICATION NUMBER: US/10/243,072
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/628,127
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 09/404,641
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-39

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGGCTGC 528
DB      1 ACTGGGCTGGGGGACTGC 18

RESULT 111
US-10-414-186-22
Sequence 22, Application US/10414186
Publication No. US20030175825A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. US20030175825A1ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/10/414,186
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US/09/404,641
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGGCTGC 528
DB      1 ACTGGGCTGGGGGACTGC 18

RESULT 112
US-10-414-186-22
Sequence 22, Application US/10414186
Publication No. US20030175825A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. US20030175825A1ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/10/414,186
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: US/09/404,641
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 22
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGGCTGC 528
DB      1 ACTGGGCTGGGGGACTGC 18

RESULT 113
US-10-659-684-23
Sequence 23, Application US/10659684
Publication No. US20040110932A1
GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Grosse, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZAPLH11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/659,684
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
```

US-10-659-684-23
; OTHER INFORMATION: Oligonucleotide primer ZC19954

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 511 ATTGGGCTGGGGGCTGC 528
|||
db 1 ACTGGGCTGGGGGACTGC 18

RESULT 114

US-09-935-868-3/c
; Sequence 3, Application US/09935868
; Patent No. US20020164690A1

```

1 / 0-935-8668-3
2 / GENERAL INFORMATION:
3 / APPLICANT: Regeneron Pharmaceuticals, Inc
4 / TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
5 / FILE REFERENCE: REG 203D
6 / CURRENT APPLICATION NUMBER: US/09/935,868
7 / CURRENT FILING DATE: 2002-04-11
8 / PRIOR APPLICATION NUMBER: PCT/US99/22045
9 / PRIOR FILING DATE: 1999-09-22
10 / NUMBER OF SEQ ID NOS: 52
11 / SOFTWARE: PatentIn version 3.0
12 / SEQ ID NO 3
13 / LENGTH: 16
14 / TYPE: DNA
15 / ORGANISM: Artificial Sequence
16 / FEATURE:
17 / OTHER INFORMATION: Kozak sequence
18 / US-09-935-8668-3

```

```
Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels
```

QY 642 CACCATGGTGACGGCG 657
|||
Db 16 CACCATGGTGCGGCG 1

RESULT 115

```

US-10-287-035-3/c
; Sequence 3, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Vancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-10-287-035-3

```

; OTHER INFORMATION
US-10-387-035-3

```

Query Match          0.9%; Score 14.4; DB 1; Length 15;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      642 CACCATGGTGACGGCG 657
          |||||
Db       16 CACCATGGTGCGGGG 1

```

RESULT 116

```

US-10-282-162-3/C
; Sequence 3, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
; US-10-282-162-3

```

```
Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 642 CACCATGGTGACGGCG 657
||| ||| ||| ||| |||
db 16 CACCATGGTGGCGCG 1

RESULT 117

US-10-138-674-5827
; Sequence 5827, Application US/10138674
; Publication No. US20040077585A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 8.2%; Pred. No. 70;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 517 CTGGGGGCCTGCACCA 532

Qy 517 CTGGGGCCTGCACCA 532

Db 1 CUGGAGCCUGCACCA 16

RESULT 118

US-10-287-949A-5827
; Sequence 5827, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 70;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTCGACCA 532

Db 1 CUGGAGCCUGCACCA 16

RESULT 119

US-09-866-108-971/c
; Sequence 971, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 971
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-971

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TTGGGCTGGGGCCTG 527

Db 17 TTGGGCTGGGGCCTG 2

RESULT 120

US-09-866-108-972/c
; Sequence 972, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 972
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-972

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TTGGGCTGGGGCCTG 527
Db 16 TTGGGCTTGGGGCCTG 1

RESULT 121
US-09-780-164-387/c
; Sequence 387, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 387
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-387

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1119 TTGGACCAGATTCA 1134
Db 17 TTGGACCAGATTGCA 2

RESULT 122
US-09-780-164-966/c
; Sequence 966, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 966
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-966

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1119 TTGGACCAGATTCA 1134

Db 16 TTGGACCAGATTGCA 1

RESULT 123
US-10-138-674-4754
; Sequence 4754, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4754

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACCA 532
Db 1 CUGGGAGCCUGCACCA 16

RESULT 124
US-10-138-674-7632
; Sequence 7632, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7632

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGGCTGCACC 531
Db 2 GCUGGGAGCCUGCACCC 17

RESULT 125
US-10-287-949A-4754
; Sequence 4754, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:

```

; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4754

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACCA 532
Db 1 CUGGAGGCCUGCACCA 16

RESULT 126
US-10-287-949A-7632
; Sequence 7632, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7632

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 79;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGCTGCACC 531
Db 2 CGUGGAGGCCUGCAC 17

RESULT 127
US-09-861-779-4/c
; Sequence 4, Application US/09861779
; Publication No. US20030191280A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: Class II Cytokine Receptor-7
; FILE REFERENCE: 96-24C2
; CURRENT APPLICATION NUMBER: US/09/861,779

```

```

; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 08/943,087
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 08/803,305
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-861-779-4

Query Match      0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470
Db 17 AAAGAGAAACACCCAG 2

RESULT 128
US-10-636-716-4/c
; Sequence 4, Application US/10636716
; Publication No. US20040072229A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/636,716
; FILING DATE: 07-AUG-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other

```

IMMEDIATE SOURCE:
CLONE: ZC11107
US-10-636-716-4

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAGAGAAAGACCCAG 1470
| | | | | | | | | | | | | | | | | | | | | |
Db 17 AAGAGAAAGACCCAG 2

RESULT 129
US-10-269-557-46
; Sequence 46, Application US/10269557
; Publication No. US2003009664A1
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/10/269,557
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/207,388
; PRIOR FILING DATE: 1998-12-08
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Used to clone Neisseria meningitidis Hsp70
; OTHER INFORMATION: gene and to construct Neisseria meningitidis Hsp70
; OTHER INFORMATION: expression vectors
US-10-269-557-46

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 AAGCAATGCTGAGGA 298
| | | | | | | | | | | | | | | | | | | | | |
Db 2 AAGCAATGCTGAGGA 17

RESULT 130
US-10-367-438-165
; Sequence 165, Application US/10367438
; Publication No. US20030180773A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, Daniel
; APPLICANT: BLUMENFELD, Marta
; APPLICANT: TCHOUMAKOV, Ilya
; TITLE OF INVENTION: Biallelic markers for use in
; TITLE OF INVENTION: constructing a high density disequilibrium map of
; TITLE OF INVENTION: the human genome.
; NUMBER OF SEQUENCES: 336
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 550 West C Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/367,438
FILING DATE: 14-Feb-2003
APPLICATION DATA:
APPLICATION NUMBER: US/09/463,075A
FILING DATE: 14-Jan-2000
INFORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: downstream amplification primer for SEQ ID15, SEQ ID65
LOCATION: 1..18
SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-10-367-438-165

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAG 1472
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AGAGAAAGACCCAG 16

RESULT 131
US-10-349-143-4102
; Sequence 4102, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density.
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4102
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13273 for SEQ 168,
US-10-349-143-4102

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTGGGGTCTCTG 16
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ATGCTGGTGTCTCTG 16

RESULT 132
US-10-349-143-9179
; Sequence 9179, Application US/10349143
; Publication No. US20040005584A1

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 6562
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-6562

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy 1058 AGCTGTGCCCTGGATA 1074
Db 1 ACCTGTGCCCTGGATA 17

RESULT 134
US-09-866-108-7084
; Sequence 7084, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752

```

; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 7084
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7084

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1502 AACCAAGGAGGAGGAGC 1518
|||
Db 1 AGCCAAAGGAGGAGGAGC 17

RESULT 135

US-09-866-108-8667
; Sequence 8667, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharon G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: ACOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Acomica Sequence Listing Engine

; SEQ ID NO 8667

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-8667

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1501 AACCAAGGAGGAGGAGC 1517
|||
Db 1 AAGCCAAAGGAGGAGGAGC 17

RESULT 136

US-09-866-108-8668

; Sequence 8668, Application US/09866108

; Patent No. US20020048800A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharon G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: ACOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 15752

; SOFTWARE: Acomica Sequence Listing Engine

; SEQ ID NO 8668

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108-8668

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1502 AACCAAGGAGGAGGAGC 1518
|||
Db 1 AGCCAAAGGAGGAGGAGC 17

RESULT 137

US-09-961-077-117

; Sequence 117, Application US/09961077

; Publication No. US20030014775A1

GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 117:
US-09-961-077-117
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 495 ACGGACATCGCCGTGAA 511
Db 1 AAGUACAUGCCCGUAA 17
RESULT 138
US-09-784-674-66/c
Sequence 66, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
Delenstarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-784-674-66
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3-GTCGTGGGTCTCTGCC 19
Db 17 GTCGTGGGTCTCTGCC 1
RESULT 139
US-09-877-478-438/c
Sequence 438, Application US/09877478
Publication No. US20030068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MEHB00-845-H (400/329)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09

```

; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 438
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-438

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1513 AGAAGCAGGAGCAAA 1529
Db 17 AGAAGTCAGAGCAAA 1

RESULT 140
US-09-848-754A-3128
; Sequence 3128, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MEHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848.754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3128
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3128

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 95;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 160 GGGATGTTGGAAATAC 176
Db 1 GGGAAUUGGAAAUUAC 17

RESULT 141
US-09-827-395A-723/c
; Sequence 723, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MEHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827.395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 723
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-723

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 542 GTCGAGGAGCATCTGGCT 558
Db 17 GTCAGCGGATCTGGCT 1

RESULT 142
US-09-740-332-1709/c
; Sequence 1709, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740.332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1709
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1709

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 292 CTGAGGAGATGACCAAG 308
Db 17 CTGAGGAGCTGGCCAAG 1

RESULT 143
US-09-740-332-1724
; Sequence 1724, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740.332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1724
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1724

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 95;

```

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1153 CCAATATGACTAACCCAG 1169
|||||:|||||
Db 1 CCAUAUAGACUCCCCAG 17

RESULT 144

US-09-740-332-2831/c
; Sequence 2831, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2831
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2831

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1154 CAATATGACTAACCCAGA 1170
|||||:|||||
Db 17 CAATATGACTCCCCAGA 1

RESULT 145

US-09-740-332-2846
; Sequence 2846, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2846
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2846

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 291 GCTGAGGAGATGACCAA 307
|||:|||||:|||||
Db 1 GCUGAGGAGCUGGCCAA 17

RESULT 146

US-09-740-332-4133

; Sequence 4133, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4133

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1267 AGGACGCCATCCCTGAG 1283
|||||:|||||
Db 1 AGGACCCACCCTGAG 17

RESULT 147

US-09-792-818-95
; Sequence 95, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-95

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 64.7%; Pred. No. 95;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1562 GGACCTCTCCAGCTCTG 1578
|||||:|||||
Db 1 GGACUUCUCCAUUCUG 17

RESULT 148

US-09-817-879-1709/c
; Sequence 1709, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879

; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1709
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1709

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 292 CTGAGGAGTGACCAAG 308
Db 17 CTGAGGAGCTGCCAAG 1

RESULT 149
US-09-817-879-1724
; Sequence 1724, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1724
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-1724

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 95;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1153 CCAATATGACTAACCAAG 1169
Db 1 CCAAAUAGACUCCCCAG 17

RESULT 150
US-09-817-879-2831/c
; Sequence 2831, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2831
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2831

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1154 CAATATGACTAACCAAG 1170
Db 17 CAATATGACTCCCCAG 1

RESULT 151
US-09-817-879-2846
; Sequence 2846, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2846
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2846

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 291 GCTGAGGAGTGACCAA 307
Db 1 GCUGAGGAGCUGGCCAA 17

RESULT 152
US-09-817-879-4133
; Sequence 4133, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4133
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4133

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1267 AGGACCCATCCCTGAG 1283


```
; ORGANISM: Homo sapiens
US-10-430-882-723

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 542 GTCCAGGACATCTGGCT 558
DB 17 GTCAGCGCATCTGGCT 1

RESULT 157
US-10-060-756A-588
; Sequence 588, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 588
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-588

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1456 AAGAGAAGACCCAGAG 1472
DB 1 AAGAGAAGACCCAGAG 17

RESULT 158
US-10-060-756A-589
; Sequence 589, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 588
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-589

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1457 AGAGAAGACCCAGAG 1473
DB 1 AGAGAAGACCCAGAG 17

RESULT 159
US-10-060-756A-590
; Sequence 590, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 590
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-590

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1458 GAGAAGACCCAGAG 1474
DB 1 GAGAAGACCCAGAG 17

RESULT 160
US-10-060-756A-591
; Sequence 591, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
```

; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: P80177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 591
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-591

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1459 AGAAGACCCAGAGGAG 1475
DB 1 AGGAAGACCTAGAGGAG 17

RESULT 161

US-10-060-998-1329/c
; Sequence 1329, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1329
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-1329

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1381 AGAGAGGAGGAGGGG 1397
DB 17 AGGAGGAGGAGGGG 1

RESULT 162

US-10-163-552-559

; Sequence 559, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to leve
; FILE REFERENCE: MEHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 559
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-559

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 95;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1315 ACAAGGCGATCGATC 1331
DB 1 ACAAGGGCAUCUGGAC 17

RESULT 163

US-10-156-306-4432/c
; Sequence 4432, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4432
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-4432

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GCCCGCTGGTGGTGGTGG 32
DB 17 GCCTGCTGGAGCTGGT 1

RESULT 164

US-10-156-306-4966/c
; Sequence 4966, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat
; FILE REFERENCE: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4966
; LENGTH: 17
; TYPE: RNA

```
; ORGANISM: Homo sapiens
US-10-156-306-4966

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 CCCGCTGGTCTGCTGT 33
Db 17 CTTGCTGGAGTCTGCT 1

RESULT 165
US-10-156-306-5928
; Sequence 5928, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5928
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5928

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 365 GGAGTACAGCAAGCAGA 381
Db 1 GGAGUACAGCAACUGA 17

RESULT 166
US-10-156-306-6988
; Sequence 6988, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6988
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6988

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1534 TCAGGAGGAGCCGAG 1550
Db 1 UGAAGGAGGAGCCGAG 17

RESULT 167
US-10-238-700-3037
; Sequence 3037, Application US/10238700
```

```
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3037
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3037

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GAGGACGAAGACGCC 1312
Db 1 GUGGACGAUACGACCC 17

RESULT 168
US-10-238-700-3128
; Sequence 3128, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/057 (MHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3128
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3128

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 95;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 658 TGGAGAGGCGCTTCTAC 674
Db 1 UGGAGGAUGCCUUCUAC 17

RESULT 169
US-10-339-782-240/c
; Sequence 240, Application US/10339782
; Publication No. US2003016026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
```


; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-240

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 AGTACTGAGAGATC 1196
DB 17 AGTTCTGAGAGATC 1

RESULT 170
US-10-297-068-971/c
; Sequence 971, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 1314OP1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 971
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: capture
US-10-297-068-971

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CACTCGGTCATCCTGAG 54
DB 17 CACTCGGTCAGCTGTG 1

RESULT 171
US-10-138-674-947
; Sequence 947, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 947
; LENGTH: 17
; TYPE: RNA

; ORGANISM: Homo sapiens
US-10-138-674-947

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 95;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAAGTCTGTGAACTT 482
DB 1 CAACUGCUUGAAACUU 17

RESULT 172
US-10-138-674-2635/c
; Sequence 2635, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2635
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2635

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGCTGCTGCTGTC 34
DB 17 CTGCTGCTGATGCTGTC 1

RESULT 173
US-10-138-674-4755
; Sequence 4755, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4755

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 95;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCTGCACCATG 534
:|||||:|||||

Db 1 UGGAGCGCCGACCAAG 17

RESULT 174

US-10-138-674-4756
; Sequence 4756, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4756
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4756

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 521 GGGCTGCACCATGCAA 537
| | | | | | | | | |
Db 1 GAGCCGACCAAGCAA 17

RESULT 175

US-10-138-674-4757
; Sequence 4757, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4757
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4757

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 523 GCGTCGACCATGCAAAG 539
| | | | | | | | | |
Db 1 GCGGACCAAGCAAAG 17

RESULT 176

US-10-138-674-4758
; Sequence 4758, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4758
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4758

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 95;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 524 CCTGCACCATGCAAAGA 540
| | | | | | | | | |
Db 1 CCUGACCAAGCAAGGA 17

RESULT 177

US-10-138-674-5394/c
; Sequence 5394, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions F
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5394
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5394

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 GTTGTGAGGACTGTCC 412
| | | | | | | | | |
Db 17 GGTGAGAGGACTGTCC 1

RESULT 178

US-10-138-674-7633
; Sequence 7633, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03

US-10-287-949A-4757
 ; Sequence 4757, Application US/10287949A
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/287,949A
 ; CURRENT FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4757
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-10-287-949A-4757

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 95;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 523 GCCTGCACCATGCAAG 539
 |||:|||||
 Db 1 GCCUGACCAAGCAAG 17

RESULT 184
 US-10-287-949A-4758
 ; Sequence 4758, Application US/10287949A
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/287,949A
 ; CURRENT FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4758
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-10-287-949A-4758

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 95;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 524 CCTGCACCATGCAAGA 540
 |||:|||||
 Db 1 CCUGACCAAGCAAG 17

RESULT 185
 US-10-287-949A-5394/c
 ; Sequence 5394, Application US/10287949A
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/287,949A
 ; CURRENT FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 5394
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-10-287-949A-5394

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 95;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 396 GTTGCTGAGGACTGTCC 412
 |||:|||||
 Db 17 GTTGAGGAGGACTGTCC 1

RESULT 186
 US-10-287-949A-7633
 ; Sequence 7633, Application US/10287949A
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions I
 ; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/287,949A
 ; CURRENT FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 7633
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-10-287-949A-7633

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 95;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 519 GGGGCGCTGCACCATGC 535
 |||:|||||
 Db 1 GGGAGCCCGCACCAAGC 17

RESULT 187
 US-10-712-672-978/c
 ; Sequence 978, Application US/10712672
 ; Publication No. US20040102413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Chowira, Bharat
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
 ; FILE REFERENCE: MHB00-882-C (400/019)
 ; CURRENT APPLICATION NUMBER: US/10/712,672
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US/09/653,225
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/197,769
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/150,713
 ; PRIOR FILING DATE: 1999-08-31

```

; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 978
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-978

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1255 AGCGATTCTCTGAGG 1269
Db 15 AGGAGATTCTCTGAGG 1

RESULT 190
US-10-287-919-1925/c
; Sequence 1925, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1925
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1144469)...(1144482)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-287-919-1925

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1255 AGCGATTCTCTGAGG 1269
Db 15 AGGAGATTCTCTGAGG 1

RESULT 191
US-09-420-433-19/c
; Sequence 19, Application US/09420433
; Patent No. US20020098480A1
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/09/420,433
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1912
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1132255)...(1132269)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-287-919-1912

```

```

; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 978
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-978

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 665 GGCCTTCTACACGAG 681
Db 17 GGCCTTCTGACACGAG 1

RESULT 188
US-10-712-672-2255/c
; Sequence 2255, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2255
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2255

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1459 AGAAGACCCGAGGAG 1475
Db 17 AGAAGACCCCTGAGCAG 1

RESULT 189
US-10-287-919-1912/c
; Sequence 1912, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1912
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1132255)...(1132269)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-287-919-1912

```

TELEPHONE: (619) 455-5100
 TELEFAX: (619) 455-5110
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..16
 US-09-420-433-19

Query Match 0.8%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 95;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 111 ATGGCGGAGGAGGAG 125
 DB 15 ATGGCGGAGGAGG 1

RESULT 192

US-09-945-505-18/c
 Sequence 18, Application US/09945505
 Publication No. US2003016584A1
 GENERAL INFORMATION:
 APPLICANT: Anastasio, Alison E.
 APPLICANT: Chew, Anne
 APPLICANT: Denton, R. Rex
 APPLICANT: Nandabalan, Krishnan
 APPLICANT: Parks, Katie E.
 APPLICANT: Stephens, J. Claiborne
 TITLE OF INVENTION: Haplotypes of the TNFRSF1A Gene
 FILE REFERENCE: MMH-00300S
 CURRENT APPLICATION NUMBER: US/09/945,505
 CURRENT FILING DATE: 2001-08-31
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 18
 LENGTH: 15
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-945-505-18

Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 94;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1331 CTGCTCCTCTGACAA 1345
 DB 15 CYGCTCCTCTGACCA 1

RESULT 193

US-10-056-414-258
 Sequence 258, Application US/10056414
 Publication No. US20030003469A1
 GENERAL INFORMATION:
 APPLICANT: Stinchcomb, Dan T.
 Draper, Kenneth G.
 McSwiggen, James
 TITLE OF INVENTION: RIBOZYME TREATMENT OF
 DISEASES OR CONDITIONS
 RELATED TO LEVELS OF
 NF-KB
 NUMBER OF SEQUENCES: 830
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles

STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/056,414
 FILING DATE: 23-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/291,932A
 FILING DATE: August 15, 1994
 APPLICATION NUMBER: 08/245,466
 FILING DATE: May 18, 1994
 APPLICATION NUMBER: 07/987,132
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/157
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 258:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 258:
 US-10-056-414-258

Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 94;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1045 GGACATATGAGAC 1057
 DB 2 GGACAUAGAGAC 14

RESULT 194

US-10-043-875-250/c
 Sequence 250, Application US/10043875
 Publication No. US20030054339A1
 GENERAL INFORMATION:
 APPLICANT: De Smet, Koenraad
 APPLICANT: Stuyver, Lieven
 TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
 Transcriptase Gene
 FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
 CURRENT APPLICATION NUMBER: US/10/043,875
 CURRENT FILING DATE: 2002-04-03
 PRIOR APPLICATION NUMBER: 60/286,102
 PRIOR FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: EP 01870085.6
 PRIOR FILING DATE: 2001-04-20
 PRIOR APPLICATION NUMBER: EP 01870005.4
 PRIOR FILING DATE: 2001-01-11
 NUMBER OF SEQ ID NOS: 884
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 250
 LENGTH: 15
 TYPE: DNA
 ORGANISM: Human immunodeficiency virus
 US-10-043-875-250

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1273 CCATCCCTGAGGA 1285
Db 15 CCATCCCTGAGGA 3

RESULT 195
US-10-101-030B-48/c
; Sequence 48, Application US/10101030B
; Publication No. US20030113738A1
; GENERAL INFORMATION:
; APPLICANT: Liu, et al.
; TITLE OF INVENTION: Evolving New Molecular Function
; FILE REFERENCE: 0342941-0071
; CURRENT APPLICATION NUMBER: US/10/101,030B
; CURRENT FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-10-101-030B-48

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CGCTGTGTGCT 31
Db 15 CGCTGTGTGCT 3

RESULT 196
US-10-084-839-3505/c
; Sequence 3505, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamachev, Victor
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Kevin L.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3505
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3505

LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3505

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CAAGCAGATGCAG 386
Db 14 CAAGCAGATGCAG 2

RESULT 197
US-10-084-839-3483/c
; Sequence 3483, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamachev, Victor
; APPLICANT: Lyamacheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Kevin L.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3483
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3483

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CAAGCAGATGCAG 386
Db 14 CAAGCAGATGCAG 2

RESULT 198
US-10-084-839-3501/c
; Sequence 3501, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Liu, et al.
; TITLE OF INVENTION: Evolving New Molecular Function
; FILE REFERENCE: 0342941-0071
; CURRENT APPLICATION NUMBER: US/10/101,030B
; CURRENT FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-10-101-030B-48

APPLICANT: Third Wave Technologies
APPLICANT: Allawi, Hatim
APPLICANT: Argue, Brad T.
APPLICANT: Bartholomay, Christian T.
APPLICANT: Chenak, LuAnne
APPLICANT: Curtis, Michelle L.
APPLICANT: Eis, Peggy S.
APPLICANT: Hall, Jeff G.
APPLICANT: Ip, Hon S.
APPLICANT: Ji, Lin
APPLICANT: Kaiser, Michael
APPLICANT: Kwiatkowski, Jr., Robert W.
APPLICANT: Lukowiak, Andrew A.
APPLICANT: Lyamichev, Victor
APPLICANT: Lymaicheva, Natalie E.
APPLICANT: Ma, WuPo
APPLICANT: Neri, Bruce P.
APPLICANT: Olson, Sarah M.
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Takova, Teetska Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Vedvik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3501
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-084-839-3501

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 374 CAAGCAGATGCAG 386
Db 13 CAAGCAGATGCAG 1

RESULT 199
US-10-277-216-330/c
Sequence 330, Application US/10277216
Publication No. US20040002470A1
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,
TITLE OF INVENTION: OBESITY, AND INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 2976-4051
CURRENT APPLICATION NUMBER: US/10/277,216
CURRENT FILING DATE: 2002-10-17
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 10/126,022
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/834,597
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/548,797
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 420
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 330
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-277-216-330

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 AGGACTGTCCAGT 415
Db 13 AGGACTGTCCAGT 1
RESULT 200
US-10-126-022-330/c
Sequence 330, Application US/10126022
Publication No. US20040023215A1
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,
TITLE OF INVENTION: OBESITY, AND INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 2976-4039US2
CURRENT APPLICATION NUMBER: US/10/126,022
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 09/834,597
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/548,797
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 420
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 330
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-126-022-330

Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 AGGACTGTCCAGT 415
Db 13 AGGACTGTCCAGT 1

RESULT 201
US-08-591-486B-124
Sequence 124, Application US/08591486B
Publication No. US20020037866A1
GENERAL INFORMATION:
APPLICANT: Schlengersiepen, Georg F
APPLICANT: Schlengersiepen, Reimar
APPLICANT: Schlengersiepen, Karl-Hermann
APPLICANT: Gotingen, Wolfgang Brysch
TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treat
TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
TITLE OF INVENTION: Treatment of Neoplasms
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh Street, N.W.
CITY: Washington, D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93111059.7
FILING DATE: 10-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 6-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10496/P60122
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-9350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-591-486B-124

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 715 GAGAGTACTTCCAGG 730
Db 1 GAGAGTACTTCTTAGG 16

RESULT 202
US-09-739-928-11
Sequence 11, Application US/09739928
Patent No. US20020052482A1
GENERAL INFORMATION:
APPLICANT: Kutyavain, Igor V.
Lukhtanov, Eugeny A.
Gamber, Howard B.
Meyer Jr., Rich B.
TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,928
FILING DATE: 11-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
APPLICATION NUMBER: US 09/507,345
FILING DATE: 18-FEB-2000
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003510US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-739-928-11

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1184 CCTGGAGAGATCAAA 1199
Db 1 CCAGCAGAGATCAAA 16

RESULT 203
US-10-339-674-569/C
Sequence 569, Application US/10339674
Publication No. US20030204318A1
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegher Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3937
SOFTWARE: Proprietary
SEQ ID NO 569
LENGTH: 16
TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
FEATURES:
LOCATION: (633528)...(633543)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 76
US-10-339-674-569

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 827 CATTTCAGCGGTC 842
Db 16 CACTTCCAGCGGTC 1

RESULT 204
US-10-059-888-22
Sequence 22, Application US/10059888
Publication No. US20030025882A1
GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULIE
APPLICANT: SONG, QING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
TITLE OF INVENTION: HYPERTENSION
FILE REFERENCE: 19113.0081U2
CURRENT APPLICATION NUMBER: US/10/059,888
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 09/495,140
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/389,566
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 08/856,141
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030025882A1e =
; OTHER INFORMATION: synthetic construct
US-10-059-888-22

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGC 1400
|||||
Db 1 GGAGGGGGGGGGGGC 16

RESULT 205

US-10-059-877-22
; Sequence 22, Application US/10059877
; Publication No. US20030157490A1
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH ESSENTIAL
; TITLE OF INVENTION: HYPERTENSION
; FILE REFERENCE: 1913.0081U2
; CURRENT APPLICATION NUMBER: US/10/059,877
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 09/495,140
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/389,566
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 08/856,141
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030157490A1e =
; OTHER INFORMATION: synthetic construct
US-10-059-877-22

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGC 1400
|||||
Db 1 GGAGGGGGGGGGGGC 16

RESULT 206

US-10-065-133A-35
; Sequence 35, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-10-065-133A-35

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 556 GCTTCTGTACGTCAA 571
|||||
Db 1 GCATCTGTTAAGTCAA 16

RESULT 207

US-10-434-811A-35
; Sequence 35, Application US/10434811A
; Publication No. US20040022809A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System of Higher
; APPLICANT: Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C1-PUS-1
; CURRENT APPLICATION NUMBER: US/10/434,811A
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-10-434-811A-35

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 556 GCTTCTGTACGTCAA 571
|||||
Db 1 GCATCTGTTAAGTCAA 16

RESULT 208

US-10-138-674-5988
; Sequence 5988, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McGswigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions i
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5988

; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5988

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGTGTGAACT 481
|||:|:|:|:|:
Db 1 CAACUGCUUGAAGCU 16

RESULT 209

US-10-287-949A-5988
; Sequence 5988, Application US/10287949A
; Publication NO. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5988
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5988

Query Match 0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGTGTGAACT 481
|||:|:|:|:|:
Db 1 CAACUGCUUGAAGCU 16

Search completed: June 24, 2004, 10:15:58
Job time : 5 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 10:19:55 / Search time 8 Seconds
(without alignments)
3.881 Million cell updates/sec

Title: US-09-817-538-2

Perfect score: 1611

Sequence: 1 atgtctggggctctgcgcg.....tcctcagctttttttccc 1611

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 449 seqs, 9636 residues

Total number of hits satisfying chosen parameters: 898

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 449 summaries

Database : rxnp2.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30.6	1.9	31	1	US-09-574-376B-170 Sequence 170, App
2	30.6	1.9	31	1	US-09-574-376B-173 Sequence 173, App
C 3	26	1.6	26	1	US-09-420-692A-47 Sequence 47, Appl
C 4	26	1.6	26	1	US-09-563-728A-4 Sequence 4, Appl
C 5	26	1.6	26	1	US-09-563-728A-13 Sequence 13, Appl
C 6	26	1.6	26	1	US-10-145-493B-47 Sequence 47, Appl
7	26	1.6	26	1	US-10-154-659-17 Sequence 17, Appl
C 8	25.2	1.6	30	1	US-10-189-818B-39 Sequence 39, Appl
9	25	1.6	25	1	US-09-396-196F-102090 Sequence 102090, App
10	25	1.6	25	1	US-09-396-196F-102091 Sequence 102091, App
11	25	1.6	25	1	US-09-396-196F-102092 Sequence 102092, App
12	25	1.6	25	1	US-09-396-196F-102093 Sequence 102093, App
13	25	1.6	25	1	US-09-396-196F-102094 Sequence 102094, App
14	25	1.6	25	1	US-09-396-196F-102095 Sequence 102095, App
15	25	1.6	25	1	US-09-396-196F-102096 Sequence 102096, App
16	25	1.6	25	1	US-09-396-196F-102097 Sequence 102097, App
17	25	1.6	25	1	US-09-396-196F-102098 Sequence 102098, App
18	25	1.6	25	1	US-09-396-196F-102099 Sequence 102099, App
19	25	1.6	25	1	US-09-396-196F-102100 Sequence 102100, App
20	25	1.6	25	1	US-09-396-196F-102101 Sequence 102101, App
21	25	1.6	25	1	US-09-396-196F-102102 Sequence 102102, App
22	25	1.6	25	1	US-09-396-196F-102103 Sequence 102103, App
23	25	1.6	25	1	US-09-396-196F-102104 Sequence 102104, App
24	25	1.6	25	1	US-09-396-196F-102105 Sequence 102105, App
25	25	1.6	25	1	US-09-396-196F-102106 Sequence 102106, App
26	25	1.6	25	1	US-09-396-196F-102107 Sequence 102107, App
27	25	1.6	25	1	US-09-396-196F-102108 Sequence 102108, App
28	25	1.6	25	1	US-09-396-196F-102109 Sequence 102109, App
29	25	1.6	25	1	US-09-396-196F-126541 Sequence 126541, App
30	25	1.6	25	1	US-09-396-196F-126542 Sequence 126542, App
31	25	1.6	25	1	US-09-396-196G-102090 Sequence 102090, App
32	25	1.6	25	1	US-09-396-196G-102091 Sequence 102091, App
33	25	1.6	25	1	US-09-396-196G-102092 Sequence 102092, App

1	US-09-396-196G-102093	25	1.6	25	Sequence 102093, App
2	US-09-396-196G-102094	25	1.6	25	Sequence 102094, App
3	US-09-396-196G-102095	25	1.6	25	Sequence 102095, App
4	US-09-396-196G-102096	25	1.6	25	Sequence 102096, App
5	US-09-396-196G-102097	25	1.6	25	Sequence 102097, App
6	US-09-396-196G-102098	25	1.6	25	Sequence 102098, App
7	US-09-396-196G-102099	25	1.6	25	Sequence 102099, App
8	US-09-396-196G-102100	25	1.6	25	Sequence 102100, App
9	US-09-396-196G-102101	25	1.6	25	Sequence 102101, App
10	US-09-396-196G-102102	25	1.6	25	Sequence 102102, App
11	US-09-396-196G-102103	25	1.6	25	Sequence 102103, App
12	US-09-396-196G-102104	25	1.6	25	Sequence 102104, App
13	US-09-396-196G-102105	25	1.6	25	Sequence 102105, App
14	US-09-396-196G-102106	25	1.6	25	Sequence 102106, App
15	US-09-396-196G-102107	25	1.6	25	Sequence 102107, App
16	US-09-396-196G-102108	25	1.6	25	Sequence 102108, App
17	US-09-396-196G-102109	25	1.6	25	Sequence 102109, App
18	US-09-396-196G-126541	25	1.6	25	Sequence 126541, App
19	US-09-396-196G-126542	25	1.6	25	Sequence 126542, App
20	US-09-953-115A-21870	25	1.6	25	Sequence 21870, App
21	US-09-953-115A-21871	25	1.6	25	Sequence 21871, App
22	US-09-953-115A-21872	25	1.6	25	Sequence 21872, App
23	US-09-953-115A-21873	25	1.6	25	Sequence 21873, App
24	US-09-953-115A-21874	25	1.6	25	Sequence 21874, App
25	US-09-953-115A-21875	25	1.6	25	Sequence 21875, App
26	US-09-953-115A-21876	25	1.6	25	Sequence 21876, App
27	US-09-953-115A-21877	25	1.6	25	Sequence 21877, App
28	US-09-953-115A-21878	25	1.6	25	Sequence 21878, App
29	US-09-953-115A-21879	25	1.6	25	Sequence 21879, App
30	US-09-953-115A-21880	25	1.6	25	Sequence 21880, App
31	US-09-953-115A-21881	25	1.6	25	Sequence 21881, App
32	US-09-953-115A-21882	25	1.6	25	Sequence 21882, App
33	US-09-953-115A-21883	25	1.6	25	Sequence 21883, App
34	US-09-953-115A-21884	25	1.6	25	Sequence 21884, App
35	US-09-953-115A-21885	25	1.6	25	Sequence 21885, App
36	US-60-507-511-94242	25	1.6	25	Sequence 94242, App
37	US-60-507-511-122445	25	1.6	25	Sequence 122445, App
38	US-60-507-511-137223	25	1.6	25	Sequence 137223, App
39	US-60-507-511-158029	25	1.6	25	Sequence 158029, App
40	US-09-420-692A-90	25	1.6	25	Sequence 90, Appl
41	US-09-563-728A-2	25	1.6	25	Sequence 2, Appl
42	US-09-563-728A-3	25	1.6	25	Sequence 3, Appl
43	US-09-563-728A-11	25	1.6	25	Sequence 11, Appl
44	US-09-563-728A-12	25	1.6	25	Sequence 12, Appl
45	US-09-396-196F-126540	25	1.6	25	Sequence 126540, App
46	US-09-396-196F-126543	25	1.6	25	Sequence 126543, App
47	US-09-396-196F-126544	25	1.6	25	Sequence 126544, App
48	US-09-396-196F-126553	25	1.6	25	Sequence 126553, App
49	US-09-396-196F-126555	25	1.6	25	Sequence 126555, App
50	US-09-396-196F-126556	25	1.6	25	Sequence 126556, App
51	US-09-396-196F-126557	25	1.6	25	Sequence 126557, App
52	US-09-396-196F-126558	25	1.6	25	Sequence 126558, App
53	US-09-396-196G-126543	25	1.6	25	Sequence 126543, App
54	US-09-396-196G-126544	25	1.6	25	Sequence 126544, App
55	US-09-396-196G-126553	25	1.6	25	Sequence 126553, App
56	US-09-396-196G-126555	25	1.6	25	Sequence 126555, App
57	US-09-396-196G-126556	25	1.6	25	Sequence 126556, App
58	US-09-396-196G-126557	25	1.6	25	Sequence 126557, App
59	US-09-396-196G-126558	25	1.6	25	Sequence 126558, App
60	US-10-719-956-181945	25	1.6	25	Sequence 181945, App
61	US-10-719-956-337747	25	1.6	25	Sequence 337747, App
62	US-60-427-836-181945	25	1.6	25	Sequence 181945, App
63	US-60-427-836-337747	25	1.6	25	Sequence 337747, App
64	US-60-507-511-59888	25	1.6	25	Sequence 59888, App
65	US-60-507-511-76813	25	1.6	25	Sequence 76813, App
66	US-60-507-511-138258	25	1.6	25	Sequence 138258, App
67	US-09-420-692A-82	25	1.6	25	Sequence 82, Appl
68	US-09-420-692A-83	25	1.6	25	Sequence 83, Appl
69	US-10-145-493B-82	25	1.6	25	Sequence 82, Appl
70	US-10-145-493B-83	25	1.6	25	Sequence 83, Appl
71	US-09-420-692A-45	25	1.6	25	Sequence 45, Appl

C 107	23	1.4	23	1	US-10-145-493B-45	Sequence 45, Appl	C 180	20	1.2	20	1	PCT-US01-46518A-13	Sequence 13, Appl
C 108	22.8	1.4	26	1	US-09-420-692A-55	Sequence 55, Appl	C 181	20	1.2	20	1	PCT-US01-46518A-14	Sequence 14, Appl
C 109	22.8	1.4	26	1	US-08-563-728A-5	Sequence 5, Appl	C 182	20	1.2	20	1	PCT-US01-46518A-15	Sequence 15, Appl
C 110	22.8	1.4	26	1	US-08-563-728A-14	Sequence 14, Appl	C 183	20	1.2	20	1	PCT-US01-46518A-16	Sequence 16, Appl
C 111	22.8	1.4	26	1	US-10-145-493B-55	Sequence 55, Appl	C 184	20	1.2	20	1	PCT-US01-46518A-17	Sequence 17, Appl
C 112	22.4	1.4	25	1	US-10-507-511-89132	Sequence 89132, A	C 185	20	1.2	20	1	PCT-US01-46518A-18	Sequence 18, Appl
C 113	22	1.4	22	1	US-08-420-692A-46	Sequence 46, Appl	C 186	20	1.2	20	1	PCT-US01-46518A-19	Sequence 19, Appl
C 114	22	1.4	22	1	US-10-145-493B-46	Sequence 46, Appl	C 187	20	1.2	20	1	PCT-US01-46518A-20	Sequence 20, Appl
C 115	21.8	1.4	25	1	US-09-396-196F-126545	Sequence 126545, A	C 188	20	1.2	20	1	PCT-US01-46518A-21	Sequence 21, Appl
C 116	21.8	1.4	25	1	US-09-396-196F-126548	Sequence 126548, A	C 189	20	1.2	20	1	PCT-US01-46518A-22	Sequence 22, Appl
C 117	21.8	1.4	25	1	US-09-396-196F-126549	Sequence 126549, A	C 190	20	1.2	20	1	PCT-US01-46518A-23	Sequence 23, Appl
C 118	21.8	1.4	25	1	US-09-396-196F-126551	Sequence 126551, A	C 191	20	1.2	20	1	PCT-US01-46518A-24	Sequence 24, Appl
C 119	21.8	1.4	25	1	US-09-396-196F-126552	Sequence 126552, A	C 192	20	1.2	20	1	PCT-US01-46518A-25	Sequence 25, Appl
C 120	21.8	1.4	25	1	US-09-396-196F-126554	Sequence 126554, A	C 193	20	1.2	20	1	PCT-US01-46518A-26	Sequence 26, Appl
C 121	21.8	1.4	25	1	US-09-396-196G-126545	Sequence 126545, A	C 194	20	1.2	20	1	PCT-US01-46518A-27	Sequence 27, Appl
C 122	21.8	1.4	25	1	US-09-396-196G-126548	Sequence 126548, A	C 195	20	1.2	20	1	PCT-US01-46518A-29	Sequence 29, Appl
C 123	21.8	1.4	25	1	US-09-396-196G-126549	Sequence 126549, A	C 196	20	1.2	20	1	PCT-US01-46518A-30	Sequence 30, Appl
C 124	21.8	1.4	25	1	US-09-396-196G-126551	Sequence 126551, A	C 197	20	1.2	20	1	PCT-US01-46518A-31	Sequence 31, Appl
C 125	21.8	1.4	25	1	US-09-396-196G-126552	Sequence 126552, A	C 198	20	1.2	20	1	PCT-US01-46518A-32	Sequence 32, Appl
C 126	21.8	1.4	25	1	US-09-396-196G-126554	Sequence 126554, A	C 199	20	1.2	20	1	PCT-US01-46518A-33	Sequence 33, Appl
C 127	21.8	1.4	25	1	US-10-719-956-181943	Sequence 181943, A	C 200	20	1.2	20	1	PCT-US01-46518A-34	Sequence 34, Appl
C 128	21.8	1.4	25	1	US-10-719-956-32416	Sequence 32416, A	C 201	20	1.2	20	1	PCT-US01-46518A-35	Sequence 35, Appl
C 129	21.8	1.4	25	1	US-10-719-956-32417	Sequence 32417, A	C 202	20	1.2	20	1	PCT-US01-46518A-36	Sequence 36, Appl
C 130	21.8	1.4	25	1	US-10-719-956-33746	Sequence 33746, A	C 203	20	1.2	20	1	PCT-US01-46518A-37	Sequence 37, Appl
C 131	21.8	1.4	25	1	US-10-719-956-417655	Sequence 417655, A	C 204	20	1.2	20	1	PCT-US01-46518A-38	Sequence 38, Appl
C 132	21.8	1.4	25	1	US-60-427-836-181943	Sequence 181943, A	C 205	20	1.2	20	1	PCT-US01-46518A-39	Sequence 39, Appl
C 133	21.8	1.4	25	1	US-60-427-836-324416	Sequence 324416, A	C 206	20	1.2	20	1	PCT-US01-46518A-40	Sequence 40, Appl
C 134	21.8	1.4	25	1	US-60-427-836-324417	Sequence 324417, A	C 207	20	1.2	20	1	PCT-US01-46518A-41	Sequence 41, Appl
C 135	21.8	1.4	25	1	US-60-427-836-337746	Sequence 337746, A	C 208	20	1.2	20	1	PCT-US01-46518A-42	Sequence 42, Appl
C 136	21.8	1.4	25	1	US-60-427-836-417655	Sequence 417655, A	C 209	20	1.2	20	1	PCT-US01-46518A-43	Sequence 43, Appl
C 137	21.8	1.4	25	1	US-60-475-871-90396	Sequence 90396, A	C 210	20	1.2	20	1	PCT-US01-46518A-44	Sequence 44, Appl
C 138	21.8	1.4	25	1	US-60-507-481-100331	Sequence 100331, A	C 211	20	1.2	20	1	PCT-US01-46518A-45	Sequence 45, Appl
C 139	21.8	1.4	25	1	US-60-507-511-67531	Sequence 67531, A	C 212	20	1.2	20	1	PCT-US01-46518A-46	Sequence 46, Appl
C 140	21.8	1.4	25	1	US-60-507-511-79042	Sequence 79042, A	C 213	20	1.2	20	1	PCT-US01-46518A-47	Sequence 47, Appl
C 141	21.8	1.4	25	1	US-60-507-511-111888	Sequence 111888, A	C 214	20	1.2	20	1	PCT-US01-46518A-48	Sequence 48, Appl
C 142	21.8	1.4	25	1	US-60-507-511-111889	Sequence 111889, A	C 215	20	1.2	20	1	PCT-US01-46518A-49	Sequence 49, Appl
C 143	21.8	1.4	25	1	US-60-507-511-147894	Sequence 147894, A	C 216	20	1.2	20	1	PCT-US01-46518A-50	Sequence 50, Appl
C 144	21.8	1.4	25	1	US-09-420-692A-89	Sequence 89, Appl	C 217	20	1.2	20	1	PCT-US01-46518A-51	Sequence 51, Appl
C 145	21.8	1.4	25	1	US-10-145-493B-89	Sequence 89, Appl	C 218	20	1.2	20	1	PCT-US01-46518A-52	Sequence 52, Appl
C 146	21.8	1.4	25	1	US-10-145-493B-89	Sequence 89, Appl	C 219	20	1.2	20	1	PCT-US01-46518A-53	Sequence 53, Appl
C 147	21.4	1.3	23	1	US-09-420-692A-53	Sequence 53, Appl	C 220	20	1.2	20	1	PCT-US01-46518A-54	Sequence 54, Appl
C 148	21.4	1.3	23	1	US-10-145-493B-53	Sequence 53, Appl	C 221	20	1.2	20	1	PCT-US01-46518A-55	Sequence 55, Appl
C 149	21.4	1.3	23	1	US-10-310-188-30105	Sequence 30105, A	C 222	20	1.2	20	1	PCT-US01-46518A-56	Sequence 56, Appl
C 150	21	1.3	21	1	US-10-154-659-16	Sequence 16, Appl	C 223	20	1.2	20	1	PCT-US01-46518A-57	Sequence 57, Appl
C 151	20.4	1.3	21	1	US-09-420-692A-54	Sequence 54, Appl	C 224	20	1.2	20	1	PCT-US01-46518A-58	Sequence 58, Appl
C 152	20.4	1.3	21	1	US-10-145-493B-54	Sequence 54, Appl	C 225	20	1.2	20	1	PCT-US01-46518A-59	Sequence 59, Appl
C 153	20.4	1.3	25	1	US-60-507-511-69977	Sequence 69977, A	C 226	20	1.2	20	1	PCT-US01-46518A-60	Sequence 60, Appl
C 154	20.2	1.3	25	1	US-09-396-196F-126539	Sequence 126539, A	C 227	20	1.2	20	1	PCT-US01-46518A-61	Sequence 61, Appl
C 155	20.2	1.3	25	1	US-09-396-196F-126546	Sequence 126546, A	C 228	20	1.2	20	1	PCT-US01-46518A-62	Sequence 62, Appl
C 156	20.2	1.3	25	1	US-09-396-196F-126547	Sequence 126547, A	C 229	20	1.2	20	1	PCT-US01-46518A-63	Sequence 63, Appl
C 157	20.2	1.3	25	1	US-09-396-196F-126550	Sequence 126550, A	C 230	20	1.2	20	1	US-09-420-692A-35	Sequence 35, Appl
C 158	20.2	1.3	25	1	US-09-396-196G-126539	Sequence 126539, A	C 231	20	1.2	20	1	US-09-420-692A-36	Sequence 36, Appl
C 159	20.2	1.3	25	1	US-09-396-196G-126546	Sequence 126546, A	C 232	20	1.2	20	1	US-09-420-692A-37	Sequence 37, Appl
C 160	20.2	1.3	25	1	US-09-396-196G-126547	Sequence 126547, A	C 233	20	1.2	20	1	US-09-420-692A-38	Sequence 38, Appl
C 161	20.2	1.3	25	1	US-09-396-196G-126550	Sequence 126550, A	C 234	20	1.2	20	1	US-09-420-692A-39	Sequence 39, Appl
C 162	20.2	1.3	25	1	US-09-954-427-71840	Sequence 71840, A	C 235	20	1.2	20	1	US-09-420-692A-41	Sequence 41, Appl
C 163	20.2	1.3	25	1	US-09-954-427A-233681	Sequence 233681, A	C 236	20	1.2	20	1	US-09-420-692A-43	Sequence 43, Appl
C 164	20.2	1.3	25	1	US-09-954-429-3060	Sequence 3060, Ap	C 237	20	1.2	20	1	US-09-420-692A-44	Sequence 44, Appl
C 165	20.2	1.3	25	1	US-10-719-956-140528	Sequence 140528, A	C 238	20	1.2	20	1	US-09-563-728A-10	Sequence 10, Appl
C 166	20.2	1.3	25	1	US-10-719-956-19560	Sequence 19560, A	C 239	20	1.2	20	1	US-09-563-728A-11	Sequence 11, Appl
C 167	20.2	1.3	25	1	US-10-719-956-356287	Sequence 356287, A	C 240	20	1.2	20	1	US-09-754-167-12	Sequence 12, Appl
C 168	20.2	1.3	25	1	US-10-719-956-417657	Sequence 417657, A	C 241	20	1.2	20	1	US-09-754-167-13	Sequence 13, Appl
C 169	20.2	1.3	25	1	US-10-719-956-444838	Sequence 444838, A	C 242	20	1.2	20	1	US-09-754-167-14	Sequence 14, Appl
C 170	20.2	1.3	25	1	US-60-233-166-71840	Sequence 71840, A	C 243	20	1.2	20	1	US-09-754-167-15	Sequence 15, Appl
C 171	20.2	1.3	25	1	US-60-427-836-140528	Sequence 140528, A	C 244	20	1.2	20	1	US-09-754-167-16	Sequence 16, Appl
C 172	20.2	1.3	25	1	US-60-427-836-19560	Sequence 19560, A	C 245	20	1.2	20	1	US-09-754-167-17	Sequence 17, Appl
C 173	20.2	1.3	25	1	US-60-427-836-356287	Sequence 356287, A	C 246	20	1.2	20	1	US-09-754-167-18	Sequence 18, Appl
C 174	20.2	1.3	25	1	US-60-427-836-417657	Sequence 417657, A	C 247	20	1.2	20	1	US-09-754-167-19	Sequence 19, Appl
C 175	20.2	1.3	25	1	US-60-427-836-444838	Sequence 444838, A	C 248	20	1.2	20	1	US-09-754-167-20	Sequence 20, Appl
C 176	20.2	1.3	25	1	US-60-507-511-178470	Sequence 178470, A	C 249	20	1.2	20	1	US-09-754-167-21	Sequence 21, Appl
C 177	20.2	1.3	25	1	US-60-507-511-178471	Sequence 178471, A	C 250	20	1.2	20	1	US-09-754-167-22	Sequence 22, Appl
C 178	20.2	1.3	25	1	PCT-US01-46518A-12	Sequence 12, Appl	C 251	20	1.2	20	1	US-09-754-167-23	Sequence 23, Appl
C 179	20	1.2	20	1			C 252	20	1.2	20	1	US-09-754-167-24	Sequence 24, Appl

```
399 14.4 0.9 1 US-10-287-949A-5927 Sequence 5827, Ap
400 14.4 0.9 1 US-10-310-188-39096 Sequence 39096, A
C 401 14.4 0.9 1 PCT-US01-23656-779 Sequence 779, App
C 402 14.4 0.9 1 PCT-US01-23656-780 Sequence 780, App
C 403 14.4 0.9 1 PCT-US02-17674-678 Sequence 678, App
C 404 14.4 0.9 1 PCT-US02-17674-678 Sequence 19155, A
C 405 14.4 0.9 1 US-09-541-946-1695 Sequence 1695, A
C 406 14.4 0.9 1 US-09-541-946-1698 Sequence 1698, Ap
C 407 14.4 0.9 1 US-09-546-745A-3282 Sequence 3282, Ap
C 408 14.4 0.9 1 US-09-546-745A-3285 Sequence 3285, Ap
C 409 14.4 0.9 1 US-09-708-690-4754 Sequence 4754, Ap
C 410 14.4 0.9 1 US-09-708-690-4754 Sequence 7632, Ap
C 411 14.4 0.9 1 US-09-780-164-387 Sequence 387, App
C 412 14.4 0.9 1 US-09-780-164-387 Sequence 966, App
C 413 14.4 0.9 1 US-09-870-161-4754 Sequence 4754, Ap
C 414 14.4 0.9 1 US-09-870-161-4754 Sequence 7632, Ap
C 415 14.4 0.9 1 US-10-138-674-4754 Sequence 4754, Ap
C 416 14.4 0.9 1 US-10-138-674-4754 Sequence 7632, Ap
C 417 14.4 0.9 1 US-10-138-674A-4754 Sequence 4754, Ap
C 418 14.4 0.9 1 US-10-138-674A-4754 Sequence 7632, Ap
C 419 14.4 0.9 1 US-10-227-563-19155 Sequence 19155, A
C 420 14.4 0.9 1 US-10-287-949A-4754 Sequence 4754, Ap
C 421 14.4 0.9 1 US-10-287-949A-4754 Sequence 7632, Ap
C 422 14.4 0.9 1 US-10-310-188-18308 Sequence 18308, A
C 423 14.4 0.9 1 US-10-367-892-19155 Sequence 19155, A
C 424 14.4 0.9 1 US-10-712-633-678 Sequence 678, App
C 425 14.4 0.9 1 US-10-723-361-971 Sequence 971, App
C 426 14.4 0.9 1 US-10-723-361-971 Sequence 972, App
C 427 14.4 0.9 1 US-60-315-676-779 Sequence 779, App
C 428 14.4 0.9 1 US-60-315-676-780 Sequence 780, App
C 429 14.4 0.9 1 US-60-339-764-2348 Sequence 2348, Ap
C 430 14.4 0.9 1 US-60-339-764-2349 Sequence 2349, Ap
C 431 14.4 0.9 1 US-08-406-779-74 Sequence 74, Appl
C 432 14.4 0.9 1 US-08-803-305-A Sequence 4, Appl
C 433 14.4 0.9 1 US-08-803-305A-4 Sequence 4, Appl
C 434 14.4 0.9 1 US-09-275-712-4 Sequence 4, Appl
C 435 14.4 0.9 1 US-09-463-075A-165 Sequence 165, App
C 436 14.4 0.9 1 US-10-269-557-46 Sequence 46, Appl
C 437 14.4 0.9 1 US-10-303-778-7630 Sequence 7630, Ap
C 438 14.4 0.9 1 US-10-303-778-8250 Sequence 8250, Ap
C 439 14.4 0.9 1 US-10-310-188-14763 Sequence 14763, A
C 440 14.4 0.9 1 US-10-310-188-18291 Sequence 18291, A
C 441 14.4 0.9 1 US-10-310-188-29093 Sequence 29093, A
C 442 14.4 0.9 1 US-10-310-188-35240 Sequence 35240, A
C 443 14.4 0.9 1 US-10-310-188-86025 Sequence 86025, A
C 444 14.4 0.9 1 US-10-310-188-86059 Sequence 86059, A
C 445 14.4 0.9 1 US-10-349-143-4102 Sequence 4102, Ap
C 446 14.4 0.9 1 US-10-349-143-5179 Sequence 5179, Ap
C 447 14.4 0.9 1 US-10-367-438-165 Sequence 165, App
C 448 14.4 0.9 1 US-10-636-716-4 Sequence 4, Appl
C 449 14.4 0.9 1 US-60-082-614-2026 Sequence 2026, Ap
```

ALIGNMENTS

```
RESULT 1
US-09-574-376B-170
; Sequence 170, Application US/09574376B
; GENERAL INFORMATION:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-574-376B-170
Query Match 1.9%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 22;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 718 AGTACTTCCAGGAAGTGGGACCTACGGGA 748
Db 1 AGTACTTCCAGGAAGTGGGACCTACGGGA 31
RESULT 2
US-09-574-376B-173
; Sequence 173, Application US/09574376B
; GENERAL INFORMATION:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-574-376B-173
Query Match 1.9%; Score 30.6; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 22;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1334 CTCCTCTGACAAACGAAATTCCTGTGAGGAA 1364
Db 1 CTCCTCTGACAAACGAAATTCCTGTGAGGAA 31
RESULT 3
US-09-420-692A-47/c
; Sequence 47, Application US/09420692A
; GENERAL INFORMATION:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
US-09-420-692A-47
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1
```

C 253	20	1.2	20	1	US-09-754-167-25	Sequence 25, Appl	326	1.1	21	1	US-08-813-159-122	Sequence 122, Appl
C 254	20	1.2	20	1	US-09-754-167-26	Sequence 26, Appl	C 327	15.8	20	1	PCT-US02-29148-65	Sequence 65, Appl
C 255	20	1.2	20	1	US-09-754-167-27	Sequence 27, Appl	C 328	15.8	20	1	US-09-514-000-14731	Sequence 14731, A
C 256	20	1.2	20	1	US-09-754-167-29	Sequence 29, Appl	C 329	15.8	20	1	US-09-953-318-65	Sequence 65, Appl
C 257	20	1.2	20	1	US-09-754-167-30	Sequence 30, Appl	C 330	15.8	20	1	US-10-446-373-65	Sequence 65, Appl
C 258	20	1.2	20	1	US-09-754-167-31	Sequence 31, Appl	C 331	15.8	21	1	US-10-310-188-35269	Sequence 35269, A
C 259	20	1.2	20	1	US-09-754-167-32	Sequence 32, Appl	C 332	15.8	21	1	US-10-751-736-12071	Sequence 12071, A
C 260	20	1.2	20	1	US-09-754-167-33	Sequence 33, Appl	C 333	15.8	21	1	US-10-751-736-28225	Sequence 28225, A
C 261	20	1.2	20	1	US-09-754-167-34	Sequence 34, Appl	C 334	15.8	21	1	US-10-751-736-28228	Sequence 28228, A
C 262	20	1.2	20	1	US-09-754-167-35	Sequence 35, Appl	C 335	15.6	17	1	PCT-US02-38147-198	Sequence 198, Appl
C 263	20	1.2	20	1	US-09-754-167-36	Sequence 36, Appl	C 336	15.6	17	1	US-09-995-529-198	Sequence 198, Appl
C 264	20	1.2	20	1	US-09-754-167-37	Sequence 37, Appl	C 337	15.6	17	1	US-10-011-250-198	Sequence 198, Appl
C 265	20	1.2	20	1	US-09-754-167-38	Sequence 38, Appl	C 338	15.4	18	1	US-10-310-188-43026	Sequence 43026, A
C 266	20	1.2	20	1	US-09-754-167-39	Sequence 39, Appl	C 339	15.4	18	1	PCT-US03-35845-27	Sequence 27, Appl
C 267	20	1.2	20	1	US-09-754-167-40	Sequence 40, Appl	C 340	15.4	20	1	PCT-US03-35845-61	Sequence 61, Appl
C 268	20	1.2	20	1	US-09-754-167-41	Sequence 41, Appl	C 341	15.4	20	1	US-08-465-866B-13	Sequence 13, Appl
C 269	20	1.2	20	1	US-09-754-167-42	Sequence 42, Appl	C 342	15.4	20	1	US-08-756-866-27	Sequence 27, Appl
C 270	20	1.2	20	1	US-09-754-167-43	Sequence 43, Appl	C 343	15.4	20	1	US-09-995-263-13	Sequence 13, Appl
C 271	20	1.2	20	1	US-09-754-167-44	Sequence 44, Appl	C 344	15.4	20	1	US-10-057-550-28	Sequence 28, Appl
C 272	20	1.2	20	1	US-09-754-167-45	Sequence 45, Appl	C 345	15.4	20	1	US-10-057-550A-27	Sequence 27, Appl
C 273	20	1.2	20	1	US-09-754-167-46	Sequence 46, Appl	C 346	15.4	20	1	US-10-173-225B-27	Sequence 27, Appl
C 274	20	1.2	20	1	US-09-754-167-47	Sequence 47, Appl	C 347	15.4	20	1	US-10-266-090-45347	Sequence 45347, A
C 275	20	1.2	20	1	US-09-754-167-48	Sequence 48, Appl	C 348	15.4	20	1	US-10-293-863-27	Sequence 27, Appl
C 276	20	1.2	20	1	US-09-754-167-49	Sequence 49, Appl	C 349	15.4	20	1	US-10-293-863-61	Sequence 61, Appl
C 277	20	1.2	20	1	US-09-754-167-50	Sequence 50, Appl	C 350	15.4	20	1	US-10-352-586-13	Sequence 13, Appl
C 278	20	1.2	20	1	US-09-754-167-51	Sequence 51, Appl	C 351	15.8	19	1	US-09-426-733-24	Sequence 24, Appl
C 279	20	1.2	20	1	US-09-754-167-52	Sequence 52, Appl	C 352	15.8	19	1	US-10-125-568-24	Sequence 24, Appl
C 280	20	1.2	20	1	US-09-754-167-54	Sequence 54, Appl	C 353	15.8	19	1	US-10-310-188-38959	Sequence 38959, A
C 281	20	1.2	20	1	US-09-754-167-55	Sequence 55, Appl	C 354	15.4	17	1	PCT-US02-25940-16869	Sequence 16869, A
C 282	20	1.2	20	1	US-09-754-167-56	Sequence 56, Appl	C 355	15.4	17	1	US-09-546-745A-3283	Sequence 3283, Ap
C 283	20	1.2	20	1	US-09-754-167-57	Sequence 57, Appl	C 356	15.4	17	1	US-09-546-745A-3284	Sequence 3284, Ap
C 284	20	1.2	20	1	US-09-754-167-58	Sequence 58, Appl	C 357	15.4	17	1	US-10-227-563-16869	Sequence 16869, A
C 285	20	1.2	20	1	US-09-754-167-59	Sequence 59, Appl	C 358	15.4	17	1	US-10-367-892-16869	Sequence 16869, A
C 286	20	1.2	20	1	US-09-754-167-60	Sequence 60, Appl	C 359	15.4	18	1	PCT-US00-00854-44	Sequence 44, Appl
C 287	20	1.2	20	1	US-09-754-167-61	Sequence 61, Appl	C 360	15.4	18	1	US-09-913-684-44	Sequence 44, Appl
C 288	20	1.2	20	1	US-09-754-167-62	Sequence 62, Appl	C 361	15.4	18	1	US-10-349-143-5052	Sequence 5052, Ap
C 289	20	1.2	20	1	US-09-754-167-63	Sequence 63, Appl	C 362	15.4	19	1	PCT-US03-05044-34	Sequence 34, Appl
C 290	20	1.2	20	1	US-09-754-167-64	Sequence 64, Appl	C 363	15.4	16	1	US-10-310-188-16111	Sequence 16111, A
C 291	20	1.2	20	1	US-09-817-538-17	Sequence 17, Appl	C 364	15	16	1	US-10-268-090-38180	Sequence 38180, A
C 292	20	1.2	20	1	US-09-817-538-18	Sequence 18, Appl	C 365	15	18	1	PCT-US00-06067-13	Sequence 23, Appl
C 293	20	1.2	20	1	US-09-817-913-17	Sequence 17, Appl	C 366	14.8	18	1	US-08-283-197B-14	Sequence 14, Appl
C 294	20	1.2	20	1	US-09-817-913-18	Sequence 18, Appl	C 367	14.8	18	1	US-09-159-254-22	Sequence 22, Appl
C 295	20	1.2	20	1	US-10-051-819B-1	Sequence 1, Appl	C 368	14.8	18	1	US-09-264-908-22	Sequence 22, Appl
C 296	20	1.2	20	1	US-10-051-819B-2	Sequence 2, Appl	C 369	14.8	18	1	US-09-264-908-22	Sequence 22, Appl
C 297	20	1.2	20	1	US-10-052-390B-1	Sequence 1, Appl	C 370	14.8	18	1	US-09-264-908-39	Sequence 39, Appl
C 298	20	1.2	20	1	US-10-052-390B-2	Sequence 2, Appl	C 371	14.8	18	1	US-09-265-117-22	Sequence 22, Appl
C 299	20	1.2	20	1	US-10-145-493B-35	Sequence 35, Appl	C 372	14.8	18	1	US-09-265-117-39	Sequence 39, Appl
C 300	20	1.2	20	1	US-10-145-493B-36	Sequence 36, Appl	C 373	14.8	18	1	US-09-265-992-23	Sequence 23, Appl
C 301	20	1.2	20	1	US-10-145-493B-37	Sequence 37, Appl	C 374	14.8	18	1	US-09-347-930-22	Sequence 22, Appl
C 302	20	1.2	20	1	US-10-145-493B-38	Sequence 38, Appl	C 375	14.8	18	1	US-09-347-930-39	Sequence 39, Appl
C 303	20	1.2	20	1	US-10-145-493B-39	Sequence 39, Appl	C 376	14.8	18	1	US-09-628-127-22	Sequence 22, Appl
C 304	20	1.2	20	1	US-10-145-493B-41	Sequence 41, Appl	C 377	14.8	18	1	US-09-628-127-39	Sequence 39, Appl
C 305	20	1.2	20	1	US-10-145-493B-43	Sequence 43, Appl	C 378	14.8	18	1	US-10-243-072-22	Sequence 22, Appl
C 306	20	1.2	20	1	US-10-145-493B-44	Sequence 44, Appl	C 379	14.8	18	1	US-10-243-072-39	Sequence 39, Appl
C 307	20	1.2	20	1	US-10-154-659-15	Sequence 15, Appl	C 380	14.8	18	1	US-10-310-188-23157	Sequence 23157, A
C 308	20	1.2	20	1	US-10-189-818B-8	Sequence 8, Appl	C 381	14.8	18	1	US-10-310-188-23178	Sequence 23178, A
C 309	20	1.2	20	1	US-10-189-818B-10	Sequence 10, Appl	C 382	14.8	18	1	US-10-310-188-58290	Sequence 58290, A
C 310	19.4	1.2	21	1	US-10-751-736-43855	Sequence 43855, A	C 383	14.8	18	1	US-10-310-188-86028	Sequence 86028, A
C 311	19.2	1.2	24	1	US-09-458-813-25	Sequence 25, Appl	C 384	14.8	18	1	US-10-414-185-22	Sequence 22, Appl
C 312	19.2	1.2	24	1	US-09-458-813-25	Sequence 25, Appl	C 385	14.8	18	1	US-10-414-185-39	Sequence 39, Appl
C 313	19.2	1.2	24	1	US-09-458-813-25	Sequence 25, Appl	C 386	14.8	18	1	US-10-659-684-23	Sequence 23, Appl
C 314	18.4	1.1	20	1	PCT-US01-46518A-28	Sequence 28, Appl	C 387	14.8	18	1	US-10-715-998-22	Sequence 22, Appl
C 315	18.4	1.1	20	1	PCT-US01-46518A-53	Sequence 53, Appl	C 388	14.8	18	1	US-10-715-998-39	Sequence 39, Appl
C 316	18.4	1.1	20	1	US-09-420-692A-40	Sequence 40, Appl	C 389	14.4	16	1	US-08-563-105-3	Sequence 3, Appl
C 317	18.4	1.1	20	1	US-09-420-692A-42	Sequence 42, Appl	C 390	14.4	16	1	US-09-177-009-3	Sequence 3, Appl
C 318	18.4	1.1	20	1	US-09-754-167-53	Sequence 28, Appl	C 391	14.4	16	1	US-09-708-690-5827	Sequence 5827, Ap
C 319	18.4	1.1	20	1	US-09-754-167-53	Sequence 28, Appl	C 392	14.4	16	1	US-09-787-835-3	Sequence 3, Appl
C 320	18.4	1.1	20	1	US-10-145-493B-40	Sequence 40, Appl	C 393	14.4	16	1	US-09-870-161-5827	Sequence 3, Appl
C 321	18.4	1.1	20	1	US-10-145-493B-42	Sequence 42, Appl	C 394	14.4	16	1	US-09-935-868-3	Sequence 3, Appl
C 322	18	1.1	18	1	US-10-154-659-12	Sequence 12, Appl	C 395	14.4	16	1	US-10-138-674-5827	Sequence 5827, Ap
C 323	17.8	1.1	21	1	US-10-751-736-43856	Sequence 43856, A	C 396	14.4	16	1	US-10-138-674A-5827	Sequence 3, Appl
C 324	17.4	1.1	20	1	US-10-266-090-51356	Sequence 51356, A	C 397	14.4	16	1	US-10-282-162-3	Sequence 3, Appl
C 325	17	1.1	21	1	PCT-US98-04571A-122	Sequence 122, App	C 398	14.4	16	1	US-10-287-035-3	Sequence 3, Appl

```
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORNE, DANIEL
; APPLICANT: BONFELS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACETYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-189-818B-39

Query Match          1.6%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 70;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1533 GTCAAGGAGGAGGCCAAGTTGGCTGAATG 1562
Db 30 GTCAAGGAGGAGGTGCGCTGGAATG 1

RESULT 9
US-09-396-196F-102090
; Sequence 102090, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102090
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102090

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AATGGAATCTATCGCCCTCACAAA 284
Db 1 AATGGAATCTATCGCCCTCACAAA 25

RESULT 10
US-09-396-196F-102091
; Sequence 102091, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
```

```
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102091

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 TGGAAATCTATCGCCCTCACAAAGC 286
Db 1 TGGAAATCTATCGCCCTCACAAAGC 25

RESULT 11
US-09-396-196F-102092
; Sequence 102092, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102092

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 GCGTCCATCGTCCAGATACATG 362
Db 1 GCGTCCATCGTCCAGATACATG 25

RESULT 12
US-09-396-196F-102093
; Sequence 102093, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102093

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


RESULT 4
US-09-563-728A-4/c
; Sequence 4, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-563-728A-4

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGATGACTCATTAATTGCTG 236
Db 26 GAATCCGATGACTCATTAATTGCTG 1

RESULT 5
US-09-563-728A-13/c
; Sequence 13, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-13

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGATGACTCATTAATTGCTG 236
Db 26 GAATCCGATGACTCATTAATTGCTG 1

RESULT 6
US-10-145-493B-47/c

; Sequence 47, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 47
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-47

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGATGACTCATTAATTGCTG 236
Db 26 GAATCCGATGACTCATTAATTGCTG 1

RESULT 7
US-10-154-659-17
; Sequence 17, Application US/10154659
; GENERAL INFORMATION:
; APPLICANT: Buxton, Francis P.
; APPLICANT: Cohen, Dalia
; APPLICANT: Fischer, Denise D
; APPLICANT: Wang, Shaowen
; TITLE OF INVENTION: Antisense oligonucleotides directed to
; FILE REFERENCE: 4-32017A
; CURRENT APPLICATION NUMBER: US/10/154,659
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/293,090
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/344,416
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/370,332
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-154-659-17

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1312 CTGACAAGCGCATCTCGATCTGCTCC 1337
Db 1 CTGACAAGCGCATCTCGATCTGCTCC 26

RESULT 8
US-10-189-818B-39/c
; Sequence 39, Application US/10189818B

QY 342 TCCATCCGTCAGATAACATGTCGG 366
Db 1 TCCATCCGTCAGATAACATGTCGG 25

RESULT 13
US-09-396-196F-102094
; Sequence 102094, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102094

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TCGTCCAGATAACATGTCGGAGTA 370
Db 1 TCGTCCAGATAACATGTCGGAGTA 25

RESULT 14
US-09-396-196F-102095
; Sequence 102095, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102095

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 CGTCCAGATAACATGTCGGAGTACA 372
Db 1 CGTCCAGATAACATGTCGGAGTACA 25

RESULT 15
US-09-396-196F-102096
; Sequence 102096, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102096

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 TCTGTCAGTTGTTCTACTGTTGTTTC 460
Db 1 TCTGTCAGTTGTTCTACTGTTGTTTC 25

RESULT 16
US-09-396-196F-102097
; Sequence 102097, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102097
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102097

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 TGTGTCAGTTGTTCTACTGTTGTTTCG 462
Db 1 TGTGTCAGTTGTTCTACTGTTGTTTCG 25

RESULT 17
US-09-396-196F-102098
; Sequence 102098, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0

```
; SEQ ID NO 102098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102098

Query Match
  1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 TCAGTGTCTACTGGTGTCTGTG 464
      |||
Db 1 TCAGTGTCTACTGGTGTCTGTG 25

RESULT 18
US-09-396-196F-102099
; Sequence 102099, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102099

Query Match
  1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 AGTTGTCTACTGGTGTCTGTGGC 466
      |||
Db 1 AGTTGTCTACTGGTGTCTGTGGC 25

RESULT 19
US-09-396-196F-102100
; Sequence 102100, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102100

Query Match
  1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 448 CTACTGGTGTCTGTGGCAAGTGC 472
      |||
```

```
Db 1 CTACTGGTGTCTGTGGCAAGTGC 25

RESULT 20
US-09-396-196F-102101
; Sequence 102101, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102101

Query Match
  1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 ACTGGTGTCTGTGGCAAGTGC 474
      |||
Db 1 ACTGGTGTCTGTGGCAAGTGC 25

RESULT 21
US-09-396-196F-102102
; Sequence 102102, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102102

Query Match
  1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 TCGCCCTCACAAGCCCAATGCTGAG 296
      |||
Db 1 TCGCCCTCACAAGCCCAATGCTGAG 25

RESULT 22
US-09-396-196F-102103
; Sequence 102103, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
```

```
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196F
/ CURRENT FILING DATE: 2001-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 102103
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196F-102103

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 CCTCAAGCCAAATGCTGAGGAGA 300
Db 1 CCTCAAGCCAAATGCTGAGGAGA 25

RESULT 23
US-09-396-196F-102104
/ Sequence 102104, Application US/09396196F
/ GENERAL INFORMATION:
/ APPLICANT: Michael Mittmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196F
/ CURRENT FILING DATE: 2001-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 102104
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196F-102104

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCAAATGCTGAGGAGATG 302
Db 1 TCACAAAGCCAAATGCTGAGGAGATG 25

RESULT 24
US-09-396-196F-102105
/ Sequence 102105, Application US/09396196F
/ GENERAL INFORMATION:
/ APPLICANT: Michael Mittmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196F
/ CURRENT FILING DATE: 2001-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 102105
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196F-102105

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCAAATGCTGAGGAGATG 302
Db 1 TCACAAAGCCAAATGCTGAGGAGATG 25

RESULT 25
US-09-396-196F-102106
/ Sequence 102106, Application US/09396196F
/ GENERAL INFORMATION:
/ APPLICANT: Michael Mittmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196F
/ CURRENT FILING DATE: 2001-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 102106
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196F-102106

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ACTACATTAATAATCTTGGCTCCAT 346
Db 1 ACTACATTAATAATCTTGGCTCCAT 25

RESULT 26
US-09-396-196F-102107
/ Sequence 102107, Application US/09396196F
/ GENERAL INFORMATION:
/ APPLICANT: Michael Mittmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196F
/ CURRENT FILING DATE: 2001-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 102107
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196F-102107

Query Match
Best Local Similarity 1.6%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 TTAATTTCTTGGCTCCATCGTCC 352
Db 1 TTAATTTCTTGGCTCCATCGTCC 25
```

```
RESULT 27
US-09-396-196F-102108
; Sequence 102108, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102108
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102108

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 AAATTCTTGGCTCCATCCGTCACG 354
      |||||
Db 1 AAATTCTTGGCTCCATCCGTCACG 25

RESULT 28
US-09-396-196F-102109
; Sequence 102109, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-102109

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 ATCTTGGCTCCATCCGTCACGAT 356
      |||||
Db 1 ATCTTGGCTCCATCCGTCACGAT 25

RESULT 29
US-09-396-196F-126541
; Sequence 126541, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
```

```
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126541

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 TCTTGGCCATCTCGAACTGCTAAA 604
      |||||
Db 1 TCTTGGCCATCTCGAACTGCTAAA 25

RESULT 30
US-09-396-196F-126542
; Sequence 126542, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126542
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126542

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 TGGCCATCTCGAACTGCTAAAAGTA 607
      |||||
Db 1 TGGCCATCTCGAACTGCTAAAAGTA 25

RESULT 31
US-09-396-196G-102090
; Sequence 102090, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 102090
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
```

US-09-396-196G-102090

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 AATGAAATCTATCGCCCTCACAA 284
Db 1 AATGAAATCTATCGCCCTCACAA 25

RESULT 32

US-09-396-196G-102091
; Sequence 102091, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102091

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 TCGAAATCTATCGCCCTCAAAAGC 286
Db 1 TCGAAATCTATCGCCCTCAAAAGC 25

RESULT 33

US-09-396-196G-102092
; Sequence 102092, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102092
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102092

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 GGGCTCCATCGTCCGATCAATG 362
Db 1 GGGCTCCATCGTCCGATCAATG 25

RESULT 34

US-09-396-196G-102093
; Sequence 102093, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102093

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TCCATCGTCCAGATAACATGTCGG 366
Db 1 TCCATCGTCCAGATAACATGTCGG 25

RESULT 35

US-09-396-196G-102094
; Sequence 102094, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102094

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TCCGTCAGATAACATGTCGGAGTA 370
Db 1 TCCGTCAGATAACATGTCGGAGTA 25

RESULT 36

US-09-396-196G-102095
; Sequence 102095, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G

```

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      438  TGCAGTTGTCTACTGGTGGTTCTG 462
DB      1  TGTCAAGTTGTCTACTGGTGGTTCTG 25

RESULT 39
US-09-396-196G-102098
; Sequence 102098, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102098
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102098

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      440  TCAGTTGTCTACTGGTGGTTCTCTG 464
DB      1  TCAGTTGTCTACTGGTGGTTCTCTG 25

RESULT 40
US-09-396-196G-102099
; Sequence 102099, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102099

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      442  AGCTGTCTACTGGTGGTTCTGTGGC 466
DB      1  AGTTGTCTACTGGTGGTTCTGTGGC 25

RESULT 41
US-09-396-196G-102100

```

```

; Sequence 102100, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102100

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      448 CTACTGGTGGTCTGTGGCAAGTGC 472
Db      1 CTACTGGTGGTCTGTGGCAAGTGC 25

RESULT 42
US-09-396-196G-102101
; Sequence 102101, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102101
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102101

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      450 ACTGGTGGTCTGTGGCAAGTGTG 474
Db      1 ACTGGTGGTCTGTGGCAAGTGTG 25

RESULT 43
US-09-396-196G-102102
; Sequence 102102, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678

```

```

; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102102

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      272 TCGCCTTCACAAAGCCAAATGCTGAG 296
Db      1 TCGCCTTCACAAAGCCAAATGCTGAG 25

RESULT 44
US-09-396-196G-102103
; Sequence 102103, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102103

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      276 CCTCACAAGCCAAATGCTGAGGAGA 300
Db      1 CCTCACAAGCCAAATGCTGAGGAGA 25

RESULT 45
US-09-396-196G-102104
; Sequence 102104, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102104

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;

```


Thu Jun 24 10:30:10 2004

```
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAAGCCAAATGCTGAGGAGATG 302
Db 1 TCACAAAGCCAAATGCTGAGGAGATG 25

RESULT 46
US-09-396-196G-102105
; Sequence 102105, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102105

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 ACCACAGCGGAGTACTACATTAAT 334
Db 1 ACCACAGCGGAGTACTACATTAAT 25

RESULT 47
US-09-396-196G-102106
; Sequence 102106, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102106
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102106

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ACTACATTAAATCTTGGCTCCAT 346
Db 1 ACTACATTAAATCTTGGCTCCAT 25

RESULT 48
US-09-396-196G-102107
; Sequence 102107, Application US/09396196G
; GENERAL INFORMATION:
```

```
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102107

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 TTAATTTCTTGGCTCCATCGTCC 352
Db 1 TTAATTTCTTGGCTCCATCGTCC 25

RESULT 49
US-09-396-196G-102108
; Sequence 102108, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102108
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102108

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 AAATTTCTTGGCTCCATCGTCCAG 354
Db 1 AAATTTCTTGGCTCCATCGTCCAG 25

RESULT 50
US-09-396-196G-102109
; Sequence 102109, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102109

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 ATTCTGGCTCCATCCCTCCAGAT 356
Db 1 ATTCTGGCTCCATCCCTCCAGAT 25

RESULT 51
US-09-396-196G-126541
; Sequence 126541, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126541

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 TCTTGCCATCTCTGGAAGTCTAA 604
Db 1 TCTTGCCATCTCTGGAAGTCTAA 25

RESULT 52
US-09-396-196G-126542
; Sequence 126542, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126542
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126542

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 TGGCCATCTCTGGAAGTCTAAAGTA 607
Db 1 TGGCCATCTCTGGAAGTCTAAAGTA 25

RESULT 53
US-09-953-115A-21870
; Sequence 21870, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21870

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAGACGACCTGACAGCG 1321
Db 1 AGGACGAGACGACCTGACAGCG 25

RESULT 54
US-09-953-115A-21871
; Sequence 21871, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21871
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21871

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1312 CTGACAGCGCATCTCGATCTGCTC 1336
Db 1 CTGACAGCGCATCTCGATCTGCTC 25

RESULT 55
US-09-953-115A-21872
; Sequence 21872, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102109
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-102109

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 ATTCTGGCTCCATCCCTCCAGAT 356
Db 1 ATTCTGGCTCCATCCCTCCAGAT 25

RESULT 51
US-09-396-196G-126541
; Sequence 126541, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126541
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126541

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 TCTTGCCATCTCTGGAAGTCTAA 604
Db 1 TCTTGCCATCTCTGGAAGTCTAA 25

RESULT 52
US-09-396-196G-126542
; Sequence 126542, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126542
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126542

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 583 TGGCCATCTCTGGAAGTCTAAAGTA 607
Db 1 TGGCCATCTCTGGAAGTCTAAAGTA 25

RESULT 53
US-09-953-115A-21870
; Sequence 21870, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21870

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAGACGACCTGACAGCG 1321
Db 1 AGGACGAGACGACCTGACAGCG 25

RESULT 54
US-09-953-115A-21871
; Sequence 21871, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21871
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21871

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1312 CTGACAGCGCATCTCGATCTGCTC 1336
Db 1 CTGACAGCGCATCTCGATCTGCTC 25

RESULT 55
US-09-953-115A-21872
; Sequence 21872, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21872
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21872

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1324 TCTGATCTGCTCTGCAACG 1348
      |||||
Db 1 TCTGATCTGCTCTGCAACG 25

RESULT 56
US-09-953-115A-21873
; Sequence 21873, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21873

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCTGTGAGGAGGATCTCG 1374
      |||||
Db 1 ATTGCTGTGAGGAGGATCTCG 25

RESULT 57
US-09-953-115A-21874
; Sequence 21874, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21874
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21874

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1555 CTTGAATGACCTCTCCAGCTCTGG 1579
      |||||
Db 1 CTTGAATGACCTCTCCAGCTCTGG 25
```

RESULT 58

```
US-09-953-115A-21876
; Sequence 21876, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21876
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21876

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 CTCTGACAAACGAATTCCTGTGAG 1361
      |||||
Db 1 CTCTGACAAACGAATTCCTGTGAG 25

RESULT 59
US-09-953-115A-21877
; Sequence 21877, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21877
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21877

Query Match          1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1074 ACGGAGATCCCTAATGAGCTTCCAT 1098
      |||||
Db 1 ACGGAGATCCCTAATGAGCTTCCAT 25

RESULT 60
US-09-953-115A-21878
; Sequence 21878, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21878
```

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1210 TTGAGAACCTTAGAATGCTGCGCA 1234
|||||
DB 1 TTGAGAACCTTAGAATGCTGCGCA 25

RESULT 61
US-09-953-115A-21879
; Sequence 21879, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21879
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21879

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 982 TTAACCTGCCTATGCTGCTGGG 1006
|||||
DB 1 TTAACCTGCCTATGCTGCTGGG 25

RESULT 62
US-09-953-115A-21880
; Sequence 21880, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21880
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21880

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1094 TCATACAAATGACTACTTGAATAC 1118
|||||
DB 1 TCATACAAATGACTACTTGAATAC 25

RESULT 63
US-09-953-115A-21881
; Sequence 21881, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1

; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21881
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21881

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 969 TTGTCAAGAGCTTTAACTGCTCA 993
|||||
DB 1 TTGTCAAGAGCTTTAACTGCTCA 25

RESULT 64
US-09-953-115A-21882
; Sequence 21882, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21882
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21882

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1131 TTCAAGCTCCACATCAGTCTCTCCA 1155
|||||
DB 1 TTCAAGCTCCACATCAGTCTCTCCA 25

RESULT 65
US-09-953-115A-21883
; Sequence 21883, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21883

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 TCCAATATGACTAACCAAGACACGA 1176

```
Db 1 TCCAAATATGACTAACCAGACACGA 25
|||||
; SEQ ID NO 94242
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-94242

RESULT 66
US-09-953-115A-21884
; Sequence 21884, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21884
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21884

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1168 AGACACGAATGACTACTCGAGAA 1192
|||||
Db 1 AGAACACGAATGACTACTCGAGAA 25

RESULT 67
US-09-953-115A-21885
; Sequence 21885, Application US/09953115A
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Analysis of Human Genes
; FILE REFERENCE: 3111.1
; CURRENT APPLICATION NUMBER: US/09/953,115A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,597
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 33029
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21885
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-953-115A-21885

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1413 TCCAACTTCAAAAAGCCCAAGAG 1437
|||||
Db 1 TCCAACTTCAAAAAGCCCAAGAG 25

RESULT 68
US-60-507-511-94242/c
; Sequence 94242, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-137223

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 TCCCACTCGGTATCCTCGAGACAC 59
|||||
Db 25 TCCCACTCGGTATCCTCGAGACAC 1

RESULT 71
US-60-507-511-158029/c
```

```
; SEQ ID NO 94242
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-94242

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 GTCATCCTGAGACACACAGCCTGAGC 68
|||||
Db 25 GTCATCCTGAGACACACAGCCTGAGC 1

RESULT 69
US-60-507-511-122445/c
; Sequence 122445, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-122445

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 TCGTGTGTCTCCCACTCGGTATC 49
|||||
Db 25 TCGTGTGTCTCCCACTCGGTATC 1

RESULT 70
US-60-507-511-137223/c
; Sequence 137223, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-137223

Query Match 1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 TCCCACTCGGTATCCTCGAGACAC 59
|||||
Db 25 TCCCACTCGGTATCCTCGAGACAC 1

RESULT 71
US-60-507-511-158029/c
```

```
; Sequence 158029, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158029
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-158029

Query Match      1.6%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ACTCGGTATCTCTGAGAACACAGCC 63
Db 25 ACTCGGTATCTCTGAGAACACAGCC 1

RESULT 72
US-09-420-692A-90/c
; Sequence 90, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-90

Query Match      1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAAATTGCTG 236
Db 25 AATCCGCATGACTCATAAATTGCTG 1

RESULT 73
US-10-145-493B-90/c
; Sequence 90, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
```

```
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-90

Query Match      1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAAATTGCTG 236
Db 25 AATCCGCATGACTCATAAATTGCTG 1

RESULT 74
US-09-563-728A-2/c
; Sequence 2, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-563-728A-2

Query Match      1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAAATTGCTG 236
Db 26 GAATCCGCATGACTCATAAATTGCTG 1

RESULT 75
US-09-563-728A-3/c
; Sequence 3, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
```

```
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-3
Query Match      1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAAATTGCTG 1

RESULT 76
US-09-563-728A-11/C
; Sequence 11, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-11
Query Match      1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAAATTGCTG 1

RESULT 77
US-09-563-728A-12/C
; Sequence 12, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-12
Query Match      1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 66;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAAATTGCTG 1

RESULT 78
US-09-396-196F-126540
; Sequence 126540, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126540
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126540
Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 ATATCGTCTTGGCCATCTCGGAAT 598
Db 1 ACATCGTCTTGGCCATCTCGGAAT 25

RESULT 79
US-09-396-196F-126543
; Sequence 126543, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126543
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126543
Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 586 CCATCTCGGAATCGCTAAAGTATCA 610
Db 1 CCATCTCGGAATCGCTAAAGTATCA 25
```

```

; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126555
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126555

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GCTTCTGTACGTCATGATCGT 580
DB 1 GCTTCTGTACGTCATGATCGT 25

RESULT 83
US-09-396-196F-126556
; Sequence 126556, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126556

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 562 GTTACGTCATGATCGCTTTGGC 586
DB 1 GTTACGTCATGATCGCTTTGGC 25

RESULT 84
US-09-396-196F-126557
; Sequence 126557, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126557
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126557

```

```

; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126555
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126555

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GCTTCTGTACGTCATGATCGT 580
DB 1 GCTTCTGTACGTCATGATCGT 25

RESULT 83
US-09-396-196F-126556
; Sequence 126556, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126556

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 562 GTTACGTCATGATCGCTTTGGC 586
DB 1 GTTACGTCATGATCGCTTTGGC 25

RESULT 84
US-09-396-196F-126557
; Sequence 126557, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126557
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126557

```



```
Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 565 ACGTCATGATGCTGCTGGCCAT 589
Db 1 ACGTCATGATGCTGCTGGCCAT 25

RESULT 85
US-09-396-196G-126558
; Sequence 126558, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126558

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 TCAATGATATGCTTGGCCATCT 592
Db 1 TCAATGATATGCTTGGCCATCT 25

RESULT 86
US-09-396-196G-126540
; Sequence 126540, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126540
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126540

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 574 ATATGCTTGGCCATCTGGAAT 598
Db 1 ACATGCTTGGCCATCTGGAAT 25

RESULT 87
US-09-396-196G-126543
; Sequence 126543, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126543
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126543

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 586 CCATCTCGAACTGCTAAAGTATCA 610
Db 1 CCATCTCGAACTGCTAAAGTATCA 25

RESULT 88
US-09-396-196G-126544
; Sequence 126544, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126544
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126544

Query Match      1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 77;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 598 TCGTAAAGTATCACCCAGAGGGTGCT 622
Db 1 TCGTAAAGTATCACCCAGAGGGTGCT 25

RESULT 89
US-09-396-196G-126553
; Sequence 126553, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
```

```
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126553

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 550 CATCGGCTCTGTTACGTCATGA 574
Db 1 CATCGGCTCTGTTACGTCATGA 25

RESULT 90
US-09-396-196G-126553
; Sequence 126553, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126553

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GCTTCTGTTACGTCATGATCGT 580
Db 1 GCTTCTGTTACGTCATGATCGT 25

RESULT 91
US-09-396-196G-126556
; Sequence 126556, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126556
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126556

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 556 GCTTCTGTTACGTCATGATCGT 580
Db 1 GCTTCTGTTACGTCATGATCGT 25

RESULT 92
US-09-396-196G-126557
; Sequence 126557, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126557
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126557

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 565 ACGTCATGATGATCGTCTTGCCAT 589
Db 1 ACGTCATGATGATCGTCTTGCCAT 25

RESULT 93
US-09-396-196G-126558
; Sequence 126558, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126558

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 TCAATGATGATCGTCTTGCCATCCT 592
Db 1 TCAATGATGATCGTCTTGCCATCCT 25

RESULT 94
US-09-396-196G-126559
; Sequence 126559, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126559
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126559

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 568 TCAATGATGATCGTCTTGCCATCCT 592
Db 1 TCAATGATGATCGTCTTGCCATCCT 25
```

; APPLICANT: Mittmann, Michael
 ; TITLE OF INVENTION: Methods of Analysis of Human Genes
 ; FILE REFERENCE: 3111.1
 ; CURRENT APPLICATION NUMBER: US/09/953,115A
 ; CURRENT FILING DATE: 2001-09-13
 ; PRIOR APPLICATION NUMBER: 60/232,597
 ; PRIOR FILING DATE: 2000-09-14
 ; NUMBER OF SEQ ID NOS: 33029
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 21875
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-953-115A-21875

Query Match 1.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 77;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1245 GTCCAAACGAGCGGATTCCTGAGG 1269
 Db 1 GTCCAAATGACGCGATTCCTGAGG 25

RESULT 95
 US-10-719-956-181945
 ; Sequence 181945, Application US/10719956
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527.1
 ; CURRENT APPLICATION NUMBER: US/10/719,956
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,836
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 181945
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-10-719-956-181945

Query Match 1.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 77;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 551 ATCTGGCTTCTGTACGTCATGAT 575
 Db 1 ATCCGGCTTCTGTACGTCATGAT 25

RESULT 96
 US-10-719-956-337747
 ; Sequence 337747, Application US/10719956
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527.1
 ; CURRENT APPLICATION NUMBER: US/10/719,956
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,836
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 337747
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-10-719-956-337747

Query Match 1.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 77;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 297 GAGATGACCAAGTACCACAGCGATG 321
 Db 1 GAGATGACCAAGTACCACAGCGACG 25

RESULT 97
 US-60-427-836-181945
 ; Sequence 181945, Application US/60427836
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527
 ; CURRENT APPLICATION NUMBER: US/60/427,836
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 181945
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-60-427-836-181945

Query Match 1.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 77;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 551 ATCTGGCTTCTGTACGTCATGAT 575
 Db 1 ATCCGGCTTCTGTACGTCATGAT 25

RESULT 98
 US-60-427-836-337747
 ; Sequence 337747, Application US/60427836
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527
 ; CURRENT APPLICATION NUMBER: US/60/427,836
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 337747
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-60-427-836-337747

Query Match 1.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 77;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 297 GAGATGACCAAGTACCACAGCGATG 321
 Db 1 GAGATGACCAAGTACCACAGCGACG 25

RESULT 99
 US-60-507-511-59988/c
 ; Sequence 59988, Application US/60507511
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
 ; FILE REFERENCE: AM 101081
 ; CURRENT APPLICATION NUMBER: US/60/507,511
 ; CURRENT FILING DATE: 2003-10-02
 ; NUMBER OF SEQ ID NOS: 203623
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 59988

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-59988

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TGAGACACAGCCTGAGGCTCTG 75
Db 25 TGAGACACAGCCTGAGGCTCTG 1

RESULT 100
US-60-507-511-76813/c
; Sequence 76813, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 76813
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-76813

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 72 TCTGTCACTCGGGTAGACACGCG 96
Db 25 TCTGTCACTCGGGTAGACACGCG 1

RESULT 101
US-60-507-511-138258/c
; Sequence 138258, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 138258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-138258

Query Match
Best Local Similarity 1.5%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 55 AACACAGCCTGAGGCTCTGTCTAC 79
Db 25 AACACAGCCTGAGGCTCTGTCTAC 1

RESULT 102
US-05-420-692A-82/c
; Sequence 82, Application US/09420692A

; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 82
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-82

Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 212 AATCCGCATGACTCATTAATTGCTG 236
Db 25 AATCCGCATGACTCATTAATTGCTG 1

RESULT 103
US-09-420-692A-83/c
; Sequence 83, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 83
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-83

Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 212 AATCCGCATGACTCATTAATTGCTG 236
Db 25 AATCCGCATGACTCATTAATTGCTG 1

RESULT 104
US-10-145-493B-82/c
; Sequence 82, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692

```
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 82
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-82

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGATGACTCATAATTGCTG 236
DB 25 AATCCGATGACCATTAATTGCTG 1

RESULT 105
US-10-145-493B-83/c
; Sequence 83, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 83
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-83

Query Match      1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 82;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGATGACTCATAATTGCTG 236
DB 25 AATCCGATGACCATTAATTGCTG 1

RESULT 106
US-09-420-692A-45/c
; Sequence 45, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 45
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-55

Query Match      1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-45

Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTACTACTACGACGG 160
DB 23 AAAGTCTGTACTACTACGACGG 1

RESULT 107
US-10-145-493B-45/c
; Sequence 45, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 45
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-45

Query Match      1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 AAAGTCTGTACTACTACGACGG 160
DB 23 AAAGTCTGTACTACTACGACGG 1

RESULT 108
US-09-420-692A-55/c
; Sequence 55, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1998-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 55
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-55

Query Match      1.4%; Score 22.8; DB 1; Length 26;
```

Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGTG 1

RESULT 109

US-09-563-728A-5/c
; Sequence 5, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-5

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGTG 1

RESULT 110

US-09-563-728A-14/c
; Sequence 14, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 23-26 are modified
; OTHER INFORMATION: Positions 1-4 and 23-26 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-22 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-14

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236

Db 26 GAATCCGCATGACCCATAACTTGTG 1

RESULT 111

US-10-145-493B-55/c
; Sequence 55, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-55

Query Match 1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACCCATAACTTGTG 1

RESULT 112

US-60-507-511-89132/c
; Sequence 89132, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 89132
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-89132

Query Match 1.4%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 96;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 60 AGCCTGAGCGCTCTGTCTACTCGG 83
Db 25 AGCCTGAGCGCTCTGTCTACTCGG 2

RESULT 113

US-09-420-692A-46/c
; Sequence 46, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William

; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-46

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAATTAATCTATTATGGACA 187
Db 22 TTGGAATTAATCTATTATGGACA 1

RESULT 114

US-10-145-493B-46/c
; Sequence 46, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-46

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAATTAATCTATTATGGACA 187
Db 22 TTGGAATTAATCTATTATGGACA 1

RESULT 115

US-09-396-196F-126545
; Sequence 126545, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126545

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 601 TAAAGTATCACCAGAGGGTGTCTA 625
Db 1 TAAAGTATCACCAGAGGGTGTCTA 25

RESULT 116

US-09-396-196F-126548
; Sequence 126548, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126548

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 634 TTGATATTCACCATGTCGATGCGGT 658
Db 1 TTGATATTCACCATGTCGATGCGGT 25

RESULT 117

US-09-396-196F-126549
; Sequence 126549, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126549

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 637 ATATTCACCATGGTACGGCGTGA 661
Db 1 ATATTCACCATGGTACGGCGTGA 25

RESULT 118
US-09-396-196F-126551
; Sequence 126551, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126551
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126551

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 TTCACCATGGTACGGCGTGAAGA 664
Db 1 TTCACCATGGTACGGCGTGAAGA 25

RESULT 119
US-09-396-196F-126552
; Sequence 126552, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126552
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126552

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 547 AGGCATCTGGCTTCTGTACGTCAA 571
Db 1 AGGCATCTGGCTTCTGTACGTCAA 25

RESULT 120
US-09-396-196F-126554
; Sequence 126554, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126554

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 601 TAAAGTATCACCAGAGGGTGTCTA 625
Db 1 TAAAGTATCACCAGAGGGTGTCTA 25

RESULT 121
US-09-396-196G-126545
; Sequence 126545, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126545
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126545

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 601 TAAAGTATCACCAGAGGGTGTCTA 625
Db 1 TAAAGTATCACCAGAGGGTGTCTA 25

RESULT 122
US-09-396-196G-126548
; Sequence 126548, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126548

```



```
; SEQ ID NO 126548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126548

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 634 TTGATATTCACCATGGTGACGGCT 658
Db 1 TTGATATTCACCATGGTGACGGCT 25

RESULT 123
US-09-396-196G-126549
; Sequence 126549, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126549
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126549

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 637 ATATTACCATGGTGACGGCTGGA 661
Db 1 ATATTACCATGGTGACGGCTGGA 25

RESULT 124
US-09-396-196G-126551
; Sequence 126551, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126551
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126551

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 640 TTCACCATGGTGACGGCTGGA 664
Db 1 TTCACCATGGTGACGGCTGGA 25

RESULT 125
US-09-396-196G-126552
; Sequence 126552, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126552
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126552

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 547 AGGCATCTGGCTTCTGTACGTCAA 571
Db 1 AAGCATCGGCTTCTGTACGTCAA 25

RESULT 126
US-09-396-196G-126554
; Sequence 126554, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126554
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126554

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 553 CTGGCTTCTGTACGTCAATGATAT 577
Db 1 CCGGCTTCTGTACGTCAATGACAT 25

RESULT 127
US-10-719-956-181943
; Sequence 181943, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
```

```
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 181943
/
/ TYPE: DNA
/ LENGTH: 25
/ ORGANISM: Rattus norvegicus
US-10-719-956-181943

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 551 ATCTGCTTCTCTGTCGTCATGAT 575
Db 1 ATCCGGCTTCTGATGTCATGAT 25

RESULT 128
US-10-719-956-324416
/ Sequence 324416, Application US/10719956
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 324416
/
/ TYPE: DNA
/ LENGTH: 25
/ ORGANISM: Rattus norvegicus
US-10-719-956-324416

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCGTGAATGGCT 518
Db 1 GACGGACATCGCGTGAATGGCT 25

RESULT 129
US-10-719-956-324417
/ Sequence 324417, Application US/10719956
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 324417
/
/ TYPE: DNA
/ LENGTH: 25
/ ORGANISM: Rattus norvegicus
US-10-719-956-324417

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCGTGAATGGCT 518
Db 1 GACGGACATCGCGTGAATGGCT 25

RESULT 130
US-10-719-956-337746
/ Sequence 337746, Application US/10719956
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 337746
/
/ TYPE: DNA
/ LENGTH: 25
/ ORGANISM: Rattus norvegicus
US-10-719-956-337746

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 GAGATGACCAAGTACACACGCGATG 321
Db 1 GAGATGACCAAGTACACACGCGAG 25

RESULT 131
US-10-719-956-417655
/ Sequence 417655, Application US/10719956
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 417655
/
/ TYPE: DNA
/ LENGTH: 25
/ ORGANISM: Rattus norvegicus
US-10-719-956-417655

Query Match          1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 659 GAGAGAGCGCTTCTACACACGCGAC 683
Db 1 GAGAGAGCGCTTCTATACCACAGAC 25

RESULT 132
US-60-427-836-181943
/ Sequence 181943, Application US/60427836
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methods of Genetic Analysis of Rat
/ FILE REFERENCE: 3527
/ CURRENT APPLICATION NUMBER: US/60/427,836
/ CURRENT FILING DATE: 2002-11-20
/ NUMBER OF SEQ ID NOS: 699466
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 181943
/
/ LENGTH: 25
```

```

; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-181943

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 551 ATCTGGCTTCTGTTACGTCATCATGAT 575
    |||||
Db 1 ATCCGGCTTCTGATACGTCATCATGAT 25

RESULT 133
US-60-427-836-324416
; Sequence 324416, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324416
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-324416

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCGTGAATGGGCT 518
    |||||
Db 1 GACGGACATCGCGTGAATGGGCT 25

RESULT 134
US-60-427-836-324417
; Sequence 324417, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-324417

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 494 GACGGACATCGCGTGAATGGGCT 518
    |||||
Db 1 GACGGACATCGCGTGAATGGGCT 25

RESULT 135
US-60-427-836-337746
; Sequence 337746, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836

```

```

; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 337746
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-337746

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 GAGATGACCAAGTACCACAGCGATG 321
    |||||
Db 1 GAGATGACCAAGTACCACAGCGATG 25

RESULT 136
US-60-427-836-417655
; Sequence 417655, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417655
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-417655

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 659 GGAAGAGGCGCTTCTACACCGGAC 683
    |||||
Db 1 GGAAGAGGCGCTTCTACACCGGAC 25

RESULT 137
US-60-475-871-90396/c
; Sequence 90396, Application US/60475871
; GENERAL INFORMATION:
; APPLICANT: Wyeth Research
; APPLICANT: Mounts, William M.
; APPLICANT: Murphy, Ellen M.
; TITLE OF INVENTION: Staphylococcus Aureus Nucleic Acid Arrays
; FILE REFERENCE: AM101085
; CURRENT APPLICATION NUMBER: US/60/475,871
; CURRENT FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 207175
; SOFTWARE: Patent version 3.1
; SEQ ID NO 90396
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-60-475-871-90396

Query Match      1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 334 TCITGGCTCCATCCGTCACAGATAA 358
    |||||
Db 25 TCITGGCTCCATCCGTCACAGATAA 1

RESULT 138

```

US-60-507-481-100331/c
; Sequence 100331, Application US/60507481
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODLES OF INFLAMMATORY DISEASES
; FILE REFERENCE: AM101084
; CURRENT APPLICATION NUMBER: US/60/507,481
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 210107
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 100331
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-60-507-481-100331

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGTCACCTCGGAGAC 57
DB 25 TCTCCCACTCGTCACCTCGGAGAC 1

RESULT 139
US-60-507-511-67531/c
; Sequence 67531, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-67531

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 TGAGCGTCTGTCTACTCGGCGTAG 88
DB 25 TGAGCGTCTGTCTACTCGGCGTAG 1

RESULT 140
US-60-507-511-79042
; Sequence 79042, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79042
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-79042

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1036 CCCGGTCTGCACATATGACAGC 1060
DB 1 CCCGGTCTGCACATATGACATC 25

RESULT 141
US-60-507-511-79043
; Sequence 79043, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79043
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-79043

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1036 CCCGGTCTGCACATATGACAGC 1060
DB 1 CCCGGTCTGCACATATGACATC 25

RESULT 142
US-60-507-511-111888
; Sequence 111888, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-111888

Query Match 1.4%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 630 GACATTGATTCACCATGGTGACG 654
DB 1 GACATTGATTCACCATGGTGACG 25

RESULT 143
US-60-507-511-111889
; Sequence 111889, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: AM 101081

; CURRENT APPLICATION NUMBER: US/60/507,511

; CURRENT FILING DATE: 2003-10-02

; NUMBER OF SEQ ID NOS: 203623

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 111889

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-507-511-111889

Query Match

Best Local Similarity 1.4%; Score 21.8; DB 1; Length 25;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 630 GACATTGATATTCACCATGGTGACG 654

Db 1 GACATTGACATCCACCATGGTGACG 25

RESULT 144

US-60-507-511-147894/c

Sequence 147894, Application US/60507511

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

FILE REFERENCE: AM 101081

CURRENT APPLICATION NUMBER: US/60/507,511

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 203623

SOFTWARE: PatentIn version 3.2

SEQ ID NO 147894

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-60-507-511-147894

Query Match

Best Local Similarity 1.4%; Score 21.8; DB 1; Length 25;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 67 GCGTCTCTGTCACCTCGGGTGACG 91

Db 25 GCGTCTCTGTCACCTCGGGTGACG 1

RESULT 145

US-09-420-692A-89/c

Sequence 89, Application US/09420692A

GENERAL INFORMATION:

APPLICANT: Besterman, Jeffrey

APPLICANT: MacLeod, Robert

APPLICANT: Siders, William

TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

FILE REFERENCE: 106101.197

CURRENT APPLICATION NUMBER: US/09/420,692A

CURRENT FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: US 60/104,804

PRIOR FILING DATE: 1998-10-19

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PatentIn version 3.0

SEQ ID NO 89

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide

US-09-420-692A-89

Query Match

Best Local Similarity 1.4%; Score 21.8; DB 1; Length 26;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 67 GCGTCTCTGTCACCTCGGGTGACG 91

Db 25 GCGTCTCTGTCACCTCGGGTGACG 1

Best Local Similarity 92.0%; Pred. No. 1.2e+02;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 212 AATCGCATGACTCATTAATTTGCTG 236

Db 25 AATCGCATGACCCATACTTGCTG 1

RESULT 146

US-10-145-493B-89/c

Sequence 89, Application US/10145493B

GENERAL INFORMATION:

APPLICANT: Besterman, Jeffrey

APPLICANT: MacLeod, Robert

APPLICANT: Siders, William

TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

FILE REFERENCE: MET-015DV

CURRENT APPLICATION NUMBER: US/10/145,493B

CURRENT FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 09/420,692

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: US 60/104,804

PRIOR FILING DATE: 1998-10-19

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PatentIn version 3.0

SEQ ID NO 89

LENGTH: 26

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer

US-10-145-493B-89

Query Match

Best Local Similarity 1.4%; Score 21.8; DB 1; Length 26;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 212 AATCGCATGACTCATTAATTTGCTG 236

Db 25 AATCGCATGACCCATACTTGCTG 1

RESULT 147

US-09-420-692A-53/c

Sequence 53, Application US/09420692A

GENERAL INFORMATION:

APPLICANT: Besterman, Jeffrey

APPLICANT: MacLeod, Robert

APPLICANT: Siders, William

TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy

FILE REFERENCE: 106101.197

CURRENT APPLICATION NUMBER: US/09/420,692A

CURRENT FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: US 60/104,804

PRIOR FILING DATE: 1998-10-19

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PatentIn version 3.0

SEQ ID NO 53

LENGTH: 23

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: oligonucleotide

US-09-420-692A-53

Query Match

Best Local Similarity 1.3%; Score 21.4; DB 1; Length 23;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTTACTACTACGACGG 160

Db 23 AAAGTCTGTTACTACTACGACGG 1

```
RESULT 148
US-10-145-493B-53/c
; Sequence 53, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-53

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCTGTACTACTACGCG 160
Db 23 AAAGTCTGTACTACTACGCG 1

RESULT 149
US-10-310-188-30105
; Sequence 30105, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-30105

Query Match 1.3%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 61 GCCTGAGCGCTCTGTCACTCGG 83
Db 1 GCCTGAGCGCTCTGTCACTCGG 23

RESULT 150
US-10-154-659-16/c
; Sequence 16, Application US/10154659
; GENERAL INFORMATION:
; APPLICANT: Buxton, Francis P.
; APPLICANT: Cohen, Dalia
; APPLICANT: Fischer, Denise D
; APPLICANT: Wang, Shaowen
; TITLE OF INVENTION: Antisense oligonucleotides directed to
; FILE REFERENCE: 4-32017A
```

```
; CURRENT APPLICATION NUMBER: US/10/154,659
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/293,090
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/344,416
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/370,332
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-154-659-16

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTCCTGTGA 1360
Db 21 TGACAAACGAATTCCTGTGA 1

RESULT 151
US-09-420-692A-54/c
; Sequence 54, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-54

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAAATTTACTATTATGGACA 187
Db 22 TTGGAAATTTACTATTATGGACA 1

RESULT 152
US-10-145-493B-54/c
; Sequence 54, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
```

; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-54

Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 166 TTGAAATTTACTATTATGACA 187
Db 22 TTGAAATTTACTATTATGACA 1

RESULT 153
US-60-507-511-69977
; Sequence 69977, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-69977

Query Match 1.3%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 GGGTCTGTACATTGACATTGA 637
Db 4 GGGTCTGTACATTGACATTGA 25

RESULT 154
US-09-396-196F-126539
; Sequence 126539, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR FILING DATE: 1998-09-17
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126539

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 541 AGTCGAGGCATCTGGCTTCGTGTTA 565
Db 1 AGTCGAGGCATCTGGCTTCGTGTTA 25

RESULT 155
US-09-396-196F-126546
; Sequence 126546, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126546

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 604 AGTATCACCAGAGGGTGTGTACAT 628
Db 1 AGTATCACCAGAGGGTGTGTATAT 25

RESULT 156
US-09-396-196F-126547
; Sequence 126547, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126547

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 607 ATCACCAGAGGGTGTGTACATTGA 631
Db 1 ACCACCAGAGGGTGTCTATATGA 25

RESULT 157
US-09-396-196F-126550
; Sequence 126550, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann

```

; SEQ ID NO 126546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126546

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 604 AGTATCACCAGAGGGTCTGTACAT 628
      |||||
Db 1 AGTATCACCAGAGGGTCTGTATAT 25

RESULT 160
US-09-396-196G-126547
; Sequence 126547, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126547

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 607 ATCCAGAGGGTCTGTACATTGA 631
      |||||
Db 1 ACCAGAGGGTCTGTATTGA 25

RESULT 161
US-09-396-196G-126550
; Sequence 126550, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126550
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126550

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 544 CCGAGCATCTGGCTTCTGTACGT 568
      |||||
Db 1 CTGAGCATCCGGCTTCTGTACGT 25
```

```

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; PRIOR FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126550
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-126550

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 544 CCGAGCATCTGGCTTCTGTACGT 568
      |||||
Db 1 CTGAGCATCCGGCTTCTGTACGT 25

RESULT 158
US-09-396-196G-126539
; Sequence 126539, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126539

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 541 AGTCCGAGGATCTGGCTTCTGTGA 565
      |||||
Db 1 AGTCTGAGCATCCGGCTTCTGTGA 25

RESULT 159
US-09-396-196G-126546
; Sequence 126546, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-126546

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 541 AGTCCGAGGATCTGGCTTCTGTGA 565
      |||||
Db 1 AGTCTGAGCATCCGGCTTCTGTGA 25
```



```

; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 3060
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429-3060

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      881  GGTCTTACAGTGTGGCTCAGACTCC 905
          |||||
DB      25  GGTCTTACAGTGTGGCAGAGGCC 1

RESULT 165
US-09-954-429B-3060/c
; Sequence 3060, Application US/09954429B
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 3060
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429B-3060

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      881  GGTCTTACAGTGTGGCTCAGACTCC 905
          |||||
DB      25  GGTCTTACAGTGTGGCAGAGGCC 1

RESULT 166
US-10-719-956-140528
; Sequence 140528, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 140528
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-140528

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      403  AGGACTGTCCAGTATTGATGCGCT 427
          |||||
DB      1    AGGACTGTCCGTATTGATGCGCT 25

; NUMBER OF SEQ ID NOS: 21305
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 3060
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-954-429-3060

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      881  GGTCTTACAGTGTGGCTCAGACTCC 905
          |||||
DB      25  GGTCTTACAGTGTGGCAGAGGCC 1

RESULT 163
US-09-954-427A-233681/c
; Sequence 233681, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 233681
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-233681

Query Match      1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1342  ACAACGAAATTCCTGTGAGGAAGA 1366
          |||||
DB      25  ACAACGAAATTCCTGTGAGGAAGA 1

RESULT 164
US-09-954-429-3060/c
; Sequence 3060, Application US/09954429
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat Neurobiology
; FILE REFERENCE: 3114.1
; CURRENT APPLICATION NUMBER: US/09/954,429
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,357
; PRIOR FILING DATE: 2000-09-18

```

RESULT 167

US-10-719-956-319560
; Sequence 319560, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-319560

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 630 GACATTGATTCACCATGTCGACG 654
|||
Db 1 GACATTGACATTCACCATGTCGATG 25
|||

RESULT 168

US-10-719-956-356287
; Sequence 356287, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356287
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-356287

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 432 GAGTTCGTGCTAGTTGCTACTGGTG 456
|||
Db 1 GAGTTCGTGCTAGTTGCTACTGGTG 25
|||

RESULT 169

US-10-719-956-417657
; Sequence 417657, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-719-956-417657

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 659 GGAAGAGGCTTCTACACCGGAC 683
|||
Db 1 GGAAGAGGCTTGTATACCAAGAC 25
|||

RESULT 170

US-10-719-956-444838
; Sequence 444838, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 444838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-444838

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 456 GGTCTGTGGCAAGTGTCTGCAAC 480
|||
Db 1 GGTCTGTGGCAAGTGTCTGCAAC 25
|||

RESULT 171

US-60-233-166-71840/c
; Sequence 71840, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819408
US-60-233-166-71840

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1342 ACAACGAATTCCTGTGAGGAAGA 1366
|||
Db 25 ACAACGAATTCCTGTGAGGAAGA 1
|||

RESULT 172

US-60-427-836-140528
; Sequence 140528, Application US/60427836
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 140528
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-140528

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 403 AGGACTGTCAGTATTCGATGGCT 427
|||||
Db 1 AGGACTGTCGGTATTGATGGCTT 25

RESULT 173
US-60-427-836-319560
; Sequence 319560, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-319560

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 630 GACATTGATATTCACCATGGTGAG 654
|||||
Db 1 GACATTGACATTCACCATGGCGATG 25

RESULT 174
US-60-427-836-356287
; Sequence 356287, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356287
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-356287

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 432 GAGTTCGTGCACTGTCTACTGGTG 456
|||||
Db 1 GAGTTCGTGCACTGTCTCCATGGGTG 25

RESULT 175
US-60-427-836-417657
; Sequence 417657, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-417657

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 659 GGAAGAGGCTTCTACACGACGAC 683
|||||
Db 1 GGAAGAGGCTTGTATACACGAC 25

RESULT 176
US-60-427-836-444838
; Sequence 444838, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 444838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-444838

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 456 GGTTCGTGCGCAAGTGTGTGAAC 480
|||||
Db 1 GGTTCGTGCGCAAGTGTGTGAAC 25

RESULT 177
US-60-507-511-178470
; Sequence 178470, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William W
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-178470

Query Match 1.3%; Score 20.2; DB 1; Length 25;

Best Local Similarity 88.0%; Pred. No. 1.5e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 670 TCTACACCGGACCGGGTCAATGAC 694
|||||
Db 1 TCTACCTCACTACCGGGTCAATGAC 25
|||||

RESULT 178
US-60-507-511-178471
; Sequence 178471, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-178471

Query Match 1.3%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 670 TCTACACCGGACCGGGTCAATGAC 694
|||||
Db 1 TCTACCTCACTACCGGGTCAATGAC 25
|||||

RESULT 179
PCT-US01-46518A-12/c
; Sequence 12, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-12

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCGGACGACAGATGCGCAGA 120
|||||
Db 20 GCGGACGACAGATGCGCAGA 1
|||||

RESULT 180
PCT-US01-46518A-13/c
; Sequence 13, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt

; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-13

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GAGGAAAGTCTGTACTACT 153
|||||
Db 20 GAGGAAAGTCTGTACTACT 1
|||||

RESULT 181
PCT-US01-46518A-14/c
; Sequence 14, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-14

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 AATTGCTGCTCAACTATGG 247
|||||
Db 20 AATTGCTGCTCAACTATGG 1
|||||

RESULT 182
PCT-US01-46518A-15/c
; Sequence 15, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA


```
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-20

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 AAGCCAATGCTGAGGAGATG 302
      |||||
Db 20 AAGCCAATGCTGAGGAGATG 1

RESULT 188
PCT-US01-46518A-21/c
; Sequence 21, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-21

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 288 AATGCTGAGGAGATGACCAA 307
      |||||
Db 20 AATGCTGAGGAGATGACCAA 1

RESULT 189
PCT-US01-46518A-22/c
; Sequence 22, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-22

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 TGAGGAGATGACCAAGTACC 312
      |||||
Db 20 TGAGGAGATGACCAAGTACC 1

RESULT 190
PCT-US01-46518A-23/c
; Sequence 23, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-23

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 TACAGCAGCAGATGCAGAG 388
      |||||
Db 20 TACAGCAGCAGATGCAGAG 1

RESULT 191
PCT-US01-46518A-24/c
; Sequence 24, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-24

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 405 GACTGTCCAGTATTCGATGG 424
      |||||
Db 20 GACTGTCCAGTATTCGATGG 1
```

```
RESULT 192
PCT-US01-46518A-25/c
; Sequence 25, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-25
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 427 TGTGAGTTCTGTCAGTTG 446
DB 20 TGTGAGTTCTGTCAGTTG 1

RESULT 193
PCT-US01-46518A-26/c
; Sequence 26, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-26
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 427 TGTGAGTTCTGTCAGTTG 446
DB 20 TGTGAGTTCTGTCAGTTG 1

RESULT 194
PCT-US01-46518A-27/c
; Sequence 27, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
```

```
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-27
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 485 TAAGCAGCAGCGGACATCG 504
DB 20 TAAGCAGCAGCGGACATCG 1

RESULT 195
PCT-US01-46518A-29/c
; Sequence 29, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-29
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 576 ATCGTCTGCGCCATCCTGGA 595
DB 20 ATCGTCTGCGCCATCCTGGA 1

RESULT 196
PCT-US01-46518A-30/c
; Sequence 30, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-30
```

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 591 CTTGCCCATCTGGAAGTGC 600
|||||
DB 20 CTTGCCCATCTGGAAGTGC 1

RESULT 197

PCT-US01-46518A-31/c
; Sequence 31, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-31

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GCGGTGGAGAGGCGCTTCTA 673
|||||
DB 20 GCGGTGGAGAGGCGCTTCTA 1

RESULT 198

PCT-US01-46518A-32/c
; Sequence 32, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-32

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 GAGGCGCTTCTACACACGGA 682
|||||
DB 20 GAGGCGCTTCTACACACGGA 1

RESULT 199

PCT-US01-46518A-33/c
; Sequence 33, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-33

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 GGAGACTACTCCCGAGAAC 733
|||||
DB 20 GGAGACTACTCCCGAGAAC 1

RESULT 200

PCT-US01-46518A-34/c
; Sequence 34, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-34

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTCCCGAGAACTGGGG 738
|||||
DB 20 GTACTCCCGAGAACTGGGG 1

RESULT 201

PCT-US01-46518A-35/c
; Sequence 35, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167


```
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-35

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 TCCAGGAAGTGGGACCTA 743
Db 20 TCCAGGAAGTGGGACCTA 1

RESULT 202
PCT-US01-46518A-36/c
; Sequence 36, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-36

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 GGAAGTGGGACCTACGGGA 748
Db 20 GGAAGTGGGACCTACGGGA 1

RESULT 203
PCT-US01-46518A-37/c
; Sequence 37, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-37
```

Query Match 1.2%; Score 20; DB 1; Length 20;

```
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-38/c
; Sequence 38, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-38

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 AGTATTATGCTGTTAACTAC 788
Db 20 AGTATTATGCTGTTAACTAC 1

RESULT 204
PCT-US01-46518A-39/c
; Sequence 39, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACGAGTCCTATGAGGCCATT 830
Db 20 ACGAGTCCTATGAGGCCATT 1

RESULT 206
PCT-US01-46518A-40/c
; Sequence 40, Application PC/TUS0146518A
```

```
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-40

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      840 GTCATGTCCAAAGTAATGA 859
Db      20 GTCATGTCCAAAGTAATGA 1

RESULT 207
PCT-US01-46518A-41/c
; Sequence 41, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      845 GTCCAAAGTAATGGAGATGT 864
Db      20 GTCCAAAGTAATGGAGATGT 1

RESULT 208
PCT-US01-46518A-42/c
; Sequence 42, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
```

```
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-42

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      850 AAGTAATGGAGATGTTCCAG 869
Db      20 AAGTAATGGAGATGTTCCAG 1

RESULT 209
PCT-US01-46518A-43/c
; Sequence 43, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-43

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      859 AGATGTTCCAGCCTAGTGGC 878
Db      20 AGATGTTCCAGCCTAGTGGC 1

RESULT 210
PCT-US01-46518A-44/c
; Sequence 44, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-44

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 905 CCTATCTGGGATCGGTAG 924
Db 20 CCTATCTGGGATCGGTAG 1

RESULT 211
PCT-US01-46518A-45/c
; Sequence 45, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-45

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 918 CGGTAGGTTCTCAATCT 937
Db 20 CGGTAGGTTCTCAATCT 1

RESULT 212
PCT-US01-46518A-46/c
; Sequence 46, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-46

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 ATCAAAGGACGCGCAAGTG 961
Db 20 ATCAAAGGACGCGCAAGTG 1

RESULT 213
PCT-US01-46518A-47/c
; Sequence 47, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-49

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1056 ACAGCTGTGGCCTGGATAC 1075
Db 20 ACAGCTGTGGCCTGGATAC 1

RESULT 216
PCT-US01-46518A-50/c
; Sequence 50, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-50

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1099 ACAATGACTACTTTGAATAC 1118
Db 20 ACAATGACTACTTTGAATAC 1

RESULT 217
PCT-US01-46518A-51/c
; Sequence 51, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-51

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1172 CACGAATGAGTACTGGAGA 1191

```

```

Db 20 CACGAATGAGTACTGGAGA 1

RESULT 218
PCT-US01-46518A-52/c
; Sequence 52, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-52

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GAGTACCTGGAGAGATCAA 1198
Db 20 GAGTACCTGGAGAGATCAA 1

RESULT 219
PCT-US01-46518A-54/c
; Sequence 54, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-54

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAGACGACCTGAC 1316
Db 20 AGGACGAGACGACCTGAC 1

RESULT 220
PCT-US01-46518A-55/c
; Sequence 55, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.

```

; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-55

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 GACCTGACAGCCCACTC 1327
DB 20 GACCTGACAGCCCACTC 1

RESULT 221
PCT-US01-46518A-56/c
; Sequence 56, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-56

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCTGTGAGGAGAGTT 1369
DB 20 ATTGCTGTGAGGAGAGTT 1

RESULT 222
PCT-US01-46518A-57/c
; Sequence 57, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-57

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1378 CTGAGAGGAGGAGAGGGG 1397
DB 20 CTGAGAGGAGGAGAGGGG 1

RESULT 223

PCT-US01-46518A-58/c
; Sequence 58, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-58

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATGAAAAAGAGAGACCC 1468
DB 20 GATGAAAAAGAGAGACCC 1

RESULT 224

PCT-US01-46518A-59/c
; Sequence 59, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-59

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GAAAACCAAGGAGGAGGC 1518
DB 20 GAAAACCAAGGAGGAGGC 1

```
RESULT 225
PCT-US01-46518A-60/c
; Sequence 60, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-60

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGGAGCCAGAA 1523
Db 20 CCAAGGAGGAGGAGCCAGAA 1

RESULT 226
PCT-US01-46518A-61/c
; Sequence 61, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-61

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 GAGGAGAGCCAGAGCCAA 1528
Db 20 GAGGAGAGCCAGAGCCAA 1

RESULT 227
PCT-US01-46518A-62/c
; Sequence 62, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
```

```
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-62

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 GAGCCGAGAGCCAAAGGGG 1533
Db 20 GAGCCGAGAGCCAAAGGGG 1

RESULT 228
PCT-US01-46518A-63/c
; Sequence 63, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-63

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAGTTGGCCTGAATGGACCT 1567
Db 20 AAGTTGGCCTGAATGGACCT 1

RESULT 229
PCT-US01-46518A-64/c
; Sequence 64, Application PC/TUS0146518A
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTSP-0227
; CURRENT APPLICATION NUMBER: PCT/US01/46518A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 09/745,167
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

PCT-US01-46518A-64

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCGGCTTCC 1584
|||||
DB 20 CCTCTCCAGCTCGGCTTCC 1

RESULT 230
US-09-420-692A-35/c
; Sequence 35, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-35

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCCGCTGGTCTGCTGCTC 36
|||||
DB 20 CCCGCTGGTCTGCTGCTC 1

RESULT 231
US-09-420-692A-36/c
; Sequence 36, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-36

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGCTCCCACTCGGTCAT 48
|||||
DB 20 GCTGCTCCCACTCGGTCAT 1

RESULT 232

US-09-420-692A-37/c
; Sequence 37, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-37

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGTCTCCCACTCGGTCATCC 50
|||||
DB 20 TGTCTCCCACTCGGTCATCC 1

RESULT 233

US-09-420-692A-38/c
; Sequence 38, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-38

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCTG 52
|||||
DB 20 TCTCCCACTCGGTCATCTG 1

RESULT 234

US-09-420-692A-39/c
; Sequence 39, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-43

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1565 CCTCTCCAGCTCTGGCTTCC 1584
          |||||
Db       20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 237
US-09-420-692A-44/c
; Sequence 44, Application US/09420692A
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: 106101.197
; CURRENT APPLICATION NUMBER: US/09/420,692A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-420-692A-44

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1585 TGCTGAGTCCCTCACGTTTC 1604
          |||||
Db       20 TGCTGAGTCCCTCACGTTTC 1

RESULT 238
US-09-563-728A-1/c
; Sequence 1, Application US/09563728A
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-1

Query Match          1.2%; Score 20; DB 1; Length 20;

```


Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCTCAGGTTTC 1604
Db 20 TGCTGAGTCCTCAGGTTTC 1

RESULT 239

US-09-754-167-12/c
Sequence 12, Application US/09754167
GENERAL INFORMATION:
APPLICANT: MacLeod, Alan R
APPLICANT: Li, Zoumei
APPLICANT: Besterman, Jeffrey M
TITLE OF INVENTION: Inhibition of Histone Deacetylase
FILE REFERENCE: 106101.229
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/132,287
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified base
LOCATION: 1-4 and 17-20 are modified
OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
OTHER INFORMATION: substituted nucleotides; positions 5-16 are
OTHER INFORMATION: deoxyribonucleotides
US-09-754-167-12

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCTCAGGTTTC 1604
Db 20 TGCTGAGTCCTCAGGTTTC 1

RESULT 240

US-09-754-167-12/c
Sequence 12, Application US/09754167
GENERAL INFORMATION:
APPLICANT: MacLeod, Alan R
APPLICANT: Li, Zoumei
APPLICANT: Besterman, Jeffrey M
TITLE OF INVENTION: Inhibition of Histone Deacetylase
FILE REFERENCE: 106101.229
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified base
LOCATION: 1-4 and 17-20 are modified
OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
OTHER INFORMATION: substituted nucleotides; positions 5-16 are
OTHER INFORMATION: deoxyribonucleotides
US-09-754-167-12

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 GCGAGCAAGATGGCGGAGA 120
Db 20 GCGAGCAAGATGGCGGAGA 1

RESULT 241

US-09-754-167-12

US-09-754-167-13/c
Sequence 13, Application US/09754167
GENERAL INFORMATION:
APPLICANT: MacLeod, Alan R
APPLICANT: Li, Zoumei
APPLICANT: Besterman, Jeffrey M
TITLE OF INVENTION: Inhibition of Histone Deacetylase
FILE REFERENCE: 106101.229
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified base
LOCATION: 1-4 and 17-20 are modified
OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
OTHER INFORMATION: substituted nucleotides; positions 5-16 are
OTHER INFORMATION: deoxyribonucleotides
US-09-754-167-13

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 GAGGAAAGTCGTTACTACT 153
Db 20 GAGGAAAGTCGTTACTACT 1

RESULT 242

US-09-754-167-14/c
Sequence 14, Application US/09754167
GENERAL INFORMATION:
APPLICANT: MacLeod, Alan R
APPLICANT: Li, Zoumei
APPLICANT: Besterman, Jeffrey M
TITLE OF INVENTION: Inhibition of Histone Deacetylase
FILE REFERENCE: 106101.229
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified base
LOCATION: 1-4 and 17-20 are modified
OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
OTHER INFORMATION: substituted nucleotides; positions 5-16 are
OTHER INFORMATION: deoxyribonucleotides
US-09-754-167-14

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 AATTGCTGCTCAACTATGG 247
Db 20 AATTGCTGCTCAACTATGG 1

RESULT 243

US-09-754-167-15/c
Sequence 15, Application US/09754167
GENERAL INFORMATION:
APPLICANT: MacLeod, Alan R
APPLICANT: Li, Zoumei
APPLICANT: Besterman, Jeffrey M
TITLE OF INVENTION: Inhibition of Histone Deacetylase
FILE REFERENCE: 106101.229
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: modified base
LOCATION: 1-4 and 17-20 are modified
OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
OTHER INFORMATION: substituted nucleotides; positions 5-16 are
OTHER INFORMATION: deoxyribonucleotides
US-09-754-167-15

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 AATTGCTGCTCAACTATGG 247
Db 20 AATTGCTGCTCAACTATGG 1

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 GCTGCTCAACTATGCTCTCT 252
DB 20 GCTGCTCAACTATGCTCTCT 1

RESULT 244
US-09-754-167-16/c
; Sequence 16, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-16

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 TCAACTATGCTCTCTACCGA 257
DB 20 TCAACTATGCTCTCTACCGA 1

RESULT 245
US-09-754-167-17/c
; Sequence 17, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-17

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATGCTCTCTACCGAAAT 262
DB 20 TATGCTCTCTACCGAAAT 1

RESULT 246
US-09-754-167-18/c
; Sequence 18, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION

FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CGCCTCACAAGCCATGCG 292
DB 20 CGCCTCACAAGCCATGCG 1

RESULT 247
US-09-754-167-19/c
; Sequence 19, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-19

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 TCACAAGCCATGCTGAGG 297
DB 20 TCACAAGCCATGCTGAGG 1

RESULT 248
US-09-754-167-20/c
; Sequence 20, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-20

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 AAGCCATGCTGAGGAGATG 302

```
Db      20 AAGCCAATGCTGAGGAGATG 1
|||||
RESULT 249
US-09-754-167-21/c
; Sequence 21, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-21
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      288 AATGCTGAGGAGATGACCAA 307
|||||
Db      20 AATGCTGAGGAGATGACCAA 1
|||||

RESULT 250
US-09-754-167-22/c
; Sequence 22, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-22
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      293 TGAGGAGATGACCAAGTACC 312
|||||
Db      20 TGAGGAGATGACCAAGTACC 1
|||||

RESULT 251
US-09-754-167-23/c
; Sequence 23, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-23
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      369 TACAGCAAGCAGATCGCAGAG 388
|||||
Db      20 TACAGCAAGCAGATCGCAGAG 1
|||||

RESULT 252
US-09-754-167-24/c
; Sequence 24, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-24
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      405 GACTGTCCAGTATTCGATGG 424
|||||
Db      20 GACTGTCCAGTATTCGATGG 1
|||||

RESULT 253
US-09-754-167-25/c
; Sequence 25, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-25
Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      427 TGTTCGAGTTCGTCTCAGTTG 446
|||||
Db      20 TGTTCGAGTTCGTCTCAGTTG 1
|||||

RESULT 254
US-09-754-167-26/c
```

```
; Sequence 26, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-26

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 480 CTTAATAAGCAGCAGCAGCGA 499
Db 20 CTTAATAAGCAGCAGCAGCGA 1

RESULT 255
US-09-754-167-27/c
; Sequence 27, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-27

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 TAAGCAGCAGCAGCAGCATCG 504
Db 20 TAAGCAGCAGCAGCAGCATCG 1

RESULT 256
US-09-754-167-29/c
; Sequence 29, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-29

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 TAAGCAGCAGCAGCAGCATCG 504
Db 20 TAAGCAGCAGCAGCAGCATCG 1

RESULT 257
US-09-754-167-30/c
; Sequence 30, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-30

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 576 ATCGCTTGGCCATCCTGGA 595
Db 20 ATCGCTTGGCCATCCTGGA 1

RESULT 258
US-09-754-167-31/c
; Sequence 31, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-31

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 CTTGGCCATCCTGGACTGC 600
Db 20 CTTGGCCATCCTGGACTGC 1

RESULT 259
US-09-754-167-32/c
; Sequence 32, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
```

```
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-32

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 GAGGCTTCTACACCGGA 682
      |||||
Db 20 GAGGCTTCTACACCGGA 1

RESULT 260
US-09-754-167-33/c
; Sequence 33, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-33

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 GGAGGTACTTCCCGAGAAC 733
      |||||
Db 20 GGAGGTACTTCCCGAGAAC 1

RESULT 261
US-09-754-167-34/c
; Sequence 34, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-34

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTTCCCGAAGTGGG 738
      |||||
```

```
Db 20 GTACTTCCCGAAGTGGG 1

RESULT 262
US-09-754-167-35/c
; Sequence 35, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-35

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 724 TCCGAGGAAGTGGGACCTA 743
      |||||
Db 20 TCCGAGGAAGTGGGACCTA 1

RESULT 263
US-09-754-167-36/c
; Sequence 36, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-36

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 GGAAGTGGGACCTACGGGA 748
      |||||
Db 20 GGAAGTGGGACCTACGGGA 1

RESULT 264
US-09-754-167-37/c
; Sequence 37, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-37

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 769 AGTATTATGCTGTAACTAC 789
DB 20 AGTATTATGCTGTAACTAC 1

RESULT 265
US-09-754-167-38/c
; Sequence 38, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-38

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 CCCGCTCCGACGGGATTG 807
DB 20 CCCGCTCCGACGGGATTG 1

RESULT 266
US-09-754-167-39/c
; Sequence 39, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 811 ACGAGTCTATGAGGCCATT 830
DB 20 ACGAGTCTATGAGGCCATT 1

RESULT 267
US-09-754-167-40/c
; Sequence 40, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-40

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 840 GTCATGTCCTCAAGTAATGGA 859
DB 20 GTCATGTCCTCAAGTAATGGA 1

RESULT 268
US-09-754-167-41/c
; Sequence 41, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-41

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 845 GTCCAAAGTAATGAGATGT 864
DB 20 GTCCAAAGTAATGAGATGT 1

RESULT 269
US-09-754-167-42/c
; Sequence 42, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-42

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULI 2/2
US-09-754-167-45/c
; Sequence 45, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODUL
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/7

```
RESULT 275
US-09-754-167-48/c
; Sequence 48, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-48

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1006 GAGCGGTGGTTACACATT 1025
Db 20 GAGCGGTGGTTACACATT 1

RESULT 276
US-09-754-167-49/c
; Sequence 49, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-49

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1056 ACAGCTGTGCCCTGGATAC 1075
Db 20 ACAGCTGTGCCCTGGATAC 1

RESULT 277
US-09-754-167-50/c
; Sequence 50, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-50

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1099 ACAATGACTACTTTGAATAC 1118
Db 20 ACAATGACTACTTTGAATAC 1

RESULT 278
US-09-754-167-51/c
; Sequence 51, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-51

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1172 CACGAATGAGTACCTGGAGA 1191
Db 20 CACGAATGAGTACCTGGAGA 1

RESULT 279
US-09-754-167-52/c
; Sequence 52, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-52

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1179 GAGTACCTGGAGAGATCAA 1198
Db 20 GAGTACCTGGAGAGATCAA 1

RESULT 280
US-09-754-167-54/c
; Sequence 54, Application US/09754167
; GENERAL INFORMATION:
```


APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 54
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-54

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAGAGACCCCTGAC 1316
DB 20 AGGACGAGAGACCCCTGAC 1

RESULT 281
US-09-754-167-55/c
Sequence 55, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 55
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-55

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 GACCTTGACAGGCGCATCTC 1327
DB 20 GACCTTGACAGGCGCATCTC 1

RESULT 282
US-09-754-167-56/c
Sequence 56, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-56

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ATTGCCTGTGAGGAGAGTT 1369
DB 20 ATTGCCTGTGAGGAGAGTT 1

RESULT 283
US-09-754-167-57/c
Sequence 57, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 57
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-57

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1378 CTGACAGAGGAGGAGGAGGG 1397
DB 20 CTGACAGAGGAGGAGGAGGG 1

RESULT 284
US-09-754-167-58/c
Sequence 58, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 58
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-58

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1449 GATGAAAAGAGAGAGAGCCC 1468
DB 20 GATGAAAAGAGAGAGAGCCC 1

RESULT 285
US-09-754-167-59/c
Sequence 59, Application US/09754167
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTS-0140
CURRENT APPLICATION NUMBER: US/09/754,167
CURRENT FILING DATE: 2000-12-19

```
/ NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-59

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 GAAACCAAGGAGGAGGAGC 1518
Db 20 GAAACCAAGGAGGAGGAGC 1

RESULT 286
US-09-754-167-60/c
; Sequence 60, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-60

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGGAGGAGC 1523
Db 20 CCAAGGAGGAGGAGGAGC 1

RESULT 287
US-09-754-167-61/c
; Sequence 61, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-61

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 GAGGAGAGCCGAGAGCCAA 1528
Db 20 GAGGAGAGCCGAGAGCCAA 1

RESULT 288
US-09-754-167-62/c
; Sequence 62, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-62

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 GAAGCCAGAGCCAGAGGGG 1533
Db 20 GAAGCCAGAGCCAGAGGGG 1

RESULT 289
US-09-754-167-63/c
; Sequence 63, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-63

Query Match          1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAGTTGGCCTGAATGGACCT 1567
Db 20 AAGTTGGCCTGAATGGACCT 1

RESULT 290
US-09-754-167-64/c
; Sequence 64, Application US/09754167
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-64

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
|||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 291

US-09-817-538-17/c
Sequence 17, Application US/09817538

GENERAL INFORMATION:

APPLICANT: Li, Zuomei

APPLICANT: Bonfils, Claire

APPLICANT: Besterman, Jeffrey

TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone

FILE REFERENCE: 106101.144

CURRENT APPLICATION NUMBER: US/09/817,538

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: US 60/192,157

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1

SEQ ID NO 17

LENGTH: 20

TYPE: DNA

ORGANISM: Human

US-09-817-538-17

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 292

US-09-817-538-18/c

Sequence 18, Application US/09817538

GENERAL INFORMATION:

APPLICANT: Li, Zuomei

APPLICANT: Bonfils, Claire

APPLICANT: Besterman, Jeffrey

TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone

FILE REFERENCE: 106101.144

CURRENT APPLICATION NUMBER: US/09/817,538

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: US 60/192,157

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1

SEQ ID NO 18

LENGTH: 20

TYPE: DNA

ORGANISM: Human

US-09-817-538-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
|||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 293

US-09-817-913-17/c

Sequence 17, Application US/09817913

GENERAL INFORMATION:

APPLICANT: Li, Zuomei

APPLICANT: Bonfils, Claire

APPLICANT: Besterman, Jeffrey

TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms

FILE REFERENCE: 106101.145

CURRENT APPLICATION NUMBER: US/09/817,913

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: US 60/192,157

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1

SEQ ID NO 17

LENGTH: 20

TYPE: DNA

ORGANISM: Human

US-09-817-913-17

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
|||
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 294

US-09-817-913-18/c

Sequence 18, Application US/09817913

GENERAL INFORMATION:

APPLICANT: Li, Zuomei

APPLICANT: Bonfils, Claire

APPLICANT: Besterman, Jeffrey

TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms

FILE REFERENCE: 106101.145

CURRENT APPLICATION NUMBER: US/09/817,913

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: US 60/192,157

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn version 3.1

SEQ ID NO 18

LENGTH: 20

TYPE: DNA

ORGANISM: Human

US-09-817-913-18

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
|||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 295

US-10-051-819B-1/c

Sequence 1, Application US/10051819B

GENERAL INFORMATION:

APPLICANT: Besterman, Jeffrey M.

APPLICANT: Bonfils, Claire

APPLICANT: Li, Zuomei

APPLICANT: Woc, Soon

APPLICANT: Vaisburg, Arkadii

APPLICANT: Delorme, Daniel

APPLICANT: Fournel, Marielle

APPLICANT: Lavoie, Rico

```
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-1

Query Match      1.2%  Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1585 TGCTGAGTCCCTCAGCTTTC 1604
Db 20 TGCTGAGTCCCTCAGCTTTC 1

RESULT 296
US-10-051-819B-2/c
; Sequence 2, Application US/10051819B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-2

Query Match      1.2%  Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 297
US-10-052-390B-1/c
; Sequence 1, Application US/10052390B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-2

Query Match      1.2%  Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 298
US-10-052-390B-2/c
; Sequence 2, Application US/10052390B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-2

Query Match      1.2%  Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 299
US-10-145-493B-35/c
; Sequence 35, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentih version 3.0
; SEQ ID NO 35
```

```
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-1

Query Match      1.2%  Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1585 TGCTGAGTCCCTCAGCTTTC 1604
Db 20 TGCTGAGTCCCTCAGCTTTC 1

RESULT 298
US-10-052-390B-2/c
; Sequence 2, Application US/10052390B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfills, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavoie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-2

Query Match      1.2%  Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 299
US-10-145-493B-35/c
; Sequence 35, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentih version 3.0
; SEQ ID NO 35
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-35

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCGCTGGTGTCTGCTGTC 36
Db 20 CCGCTGGTGTCTGTC 1

RESULT 300
US-10-145-493B-36/c
; Sequence 36, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-36

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGTCTCCCACTCGGTCA 48
Db 20 GCTGTCTCCCACTCGGTCA 1

RESULT 301
US-10-145-493B-37/c
; Sequence 37, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-37

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGTCTCCCACTCGGTCA 50
Db 20 TGTCTCCCACTCGGTCA 1

RESULT 302
US-10-145-493B-38/c
; Sequence 38, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-38

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCA 52
Db 20 TCTCCCACTCGGTCA 1

RESULT 303
US-10-145-493B-39/c
; Sequence 39, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-39

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 41 TCGTCATCTCGAGACACA 60
DB 20 TCGTCATCTCGAGACACA 1

RESULT 304

US-10-145-493B-41/c
; Sequence 41, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-41

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGGAGCCAGAA 1523
DB 20 CCAAGGAGGAGGAGCCAGAA 1

RESULT 305

US-10-145-493B-43/c
; Sequence 43, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-43

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
DB 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 306
US-10-145-493B-44/c
; Sequence 44, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-44

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
DB 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 307

US-10-154-659-15
; Sequence 15, Application US/10154659
; GENERAL INFORMATION:
; APPLICANT: Buxton, Francis P.
; APPLICANT: Cohen, Dalia
; APPLICANT: Fischer, Denise D
; APPLICANT: Wang, Shaowen
; TITLE OF INVENTION: Antisense oligonucleotides directed to
; FILE REFERENCE: 4-32017A
; CURRENT APPLICATION NUMBER: US/10/154,659
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/293,090
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/344,416
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/370,332
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-154-659-15

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 CGGATGAGGACGAGACGAC 1310
DB 1 CGGATGAGGACGAGACGAC 20

```
RESULT 308
US-10-189-818B-8/c
; Sequence 8, Application US/10189818B
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-189-818B-8
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1585 TGCTGAGTCCCTCAGGTTTC 1604
Db 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 309
US-10-189-818B-10/c
; Sequence 10, Application US/10189818B
; GENERAL INFORMATION:
; APPLICANT: BESTERMAN, JEFFREY M.
; APPLICANT: ZUOMEI, LI
; APPLICANT: DELORME, DANIEL
; APPLICANT: BONFILS, CLAIRE
; TITLE OF INVENTION: METHODS FOR SPECIFICALLY INHIBITING HISTONE DEACTYLASE-7 AND 8
; FILE REFERENCE: MET-024US1(1002/025)
; CURRENT APPLICATION NUMBER: US/10/189,818B
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-189-818B-10
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1565 CCTCTCCAGCTCTGGCTTCC 1584
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 310
US-10-751-736-43855/c
; Sequence 43855, Application US/10751736
```

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43855
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-43855
Query Match 1.2%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 1;

Qy 131 CCGGAGGAAAGTCTGTTACTA 151
Db 21 CCGGAGGAAAGTCTGTTACTA 1

RESULT 311
US-09-458-813-25/c
; Sequence 25, Application US/09458813
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skiadopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT LIVE-ATTENUATED PARAINFLUENZA VIRUS
; TITLE OF INVENTION: (PIV) AS A VECTOR TO PROTECT AGAINST DISEASE CAUSED BY
; TITLE OF INVENTION: PIV AND RESPIRATORY SYNCYTIAL VIRUS (RSV)
; FILE REFERENCE: 17634-000330
; CURRENT APPLICATION NUMBER: US/09/458,813
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 09/083,793
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/047,575
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/059,385
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: insert to conform inserted sequence to rule of
; OTHER INFORMATION: six.
US-09-458-813-25
Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 3;

Qy 633 ATTGATATTCCACCATGTCACGCG 656
Db 24 ATTGCTATTCCACCATGTCACGCG 1

RESULT 312
US-09-459-062-18/c
```

Sequence 18, Application US/09459062
GENERAL INFORMATION:
APPLICANT: Tao, Tao
APPLICANT: Skiadopoulos, Mario H.
APPLICANT: Collins, Peter L.
APPLICANT: Murphy, Brian R.
TITLE OF INVENTION: CONSTRUCTION AND USE OF RECOMBINANT PARAINFLUENZA
TITLE OF INVENTION: VIRUSES EXPRESSING A CHIMERIC GLYCOPROTEIN
FILE REFERENCE: 17634-000340US
CURRENT APPLICATION NUMBER: US/09/459,062
CURRENT FILING DATE: 2001-06-04
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 09/083,793
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059,385
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,575
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HPIV1 HN
US-09-459-062-18

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 633 ATTGATATTCCACCATGTCGACGCC 656
|||||
DB 24 ATTGCTATTCCACCATGTCGACGCC 1

RESULT 313
US-09-733-692A-24/c
Sequence 24, Application US/09733692A
GENERAL INFORMATION:
APPLICANT: Murphy, Brian R.
APPLICANT: Collins, Peter L.
APPLICANT: Schmidt, Alexander C.
APPLICANT: Durbin, Anna P.
APPLICANT: Skiadopoulos, Mario H.
APPLICANT: Tao, Tao
TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIV) AS
TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
TITLE OF INVENTION: BY PIV AND OTHER HUMAN PATHOGENS
FILE REFERENCE: 15280-404100US
CURRENT APPLICATION NUMBER: US/09/733,692A
CURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HPIV1 HN
US-09-733-692A-24

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 633 ATTGATATTCCACCATGTCGACGCC 656
|||||
DB 24 ATTGCTATTCCACCATGTCGACGCC 1

RESULT 314
PCT-US01-46518A-28/c
Sequence 28, Application PC/TUS0146518A
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
APPLICANT: ISIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTSP-0227
CURRENT APPLICATION NUMBER: PCT/US01/46518A
CURRENT FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 09/745,167
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 28
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-28

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 490 AGCAGACGGACATCGCGTG 509
|||||
DB 20 AGCAGACGGACATCGCGTG 1

RESULT 315
PCT-US01-46518A-53/c
Sequence 53, Application PC/TUS0146518A
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: ISIS PHARMACEUTICALS, INC.
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
FILE REFERENCE: RTSP-0227
CURRENT APPLICATION NUMBER: PCT/US01/46518A
CURRENT FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 09/745,167
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 53
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
PCT-US01-46518A-53

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1246 TCCAAACGACGCGATTCCT 1265
|||||
DB 20 TCCAAATGACGCGATTCCT 1

RESULT 316
US-09-420-692A-40/c
Sequence 40, Application US/09420692A
GENERAL INFORMATION:
APPLICANT: Besterman, Jeffrey
APPLICANT: MacLeod, Robert
APPLICANT: Siders, William
TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
FILE REFERENCE: 106101.197


```
/ CURRENT APPLICATION NUMBER: US/09/420,692A
/ CURRENT FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: US 60/104,804
/ PRIOR FILING DATE: 1998-10-19
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 40
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: oligonucleotide
US-09-420-692A-40

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGACGCGCTCTGTCACTC 81
Db      20 CCTGACGCGCTCTGTCACTC 1

RESULT 317
US-09-420-692A-42/c
/ Sequence 42, Application US/09420692A
/ GENERAL INFORMATION:
/ APPLICANT: Besterman, Jeffrey
/ APPLICANT: MacLeod, Robert
/ APPLICANT: Siders, William
/ TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
/ FILE REFERENCE: 106101.197
/ CURRENT APPLICATION NUMBER: US/09/420,692A
/ CURRENT FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: US 60/104,804
/ PRIOR FILING DATE: 1998-10-19
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 42
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: oligonucleotide
US-09-420-692A-42

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1531 GGGTCAGGAGGAGGCGCAAG 1550
Db      20 GGGTCAGGAGGAGGCGCAAG 1

RESULT 318
US-09-754-167-28/c
/ Sequence 28, Application US/09754167
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Jacqueline Wyatt
/ TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
/ FILE REFERENCE: RTS-0140
/ CURRENT APPLICATION NUMBER: US/09/754,167
/ CURRENT FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 87
/ SEQ ID NO 28
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-28

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGACGCGCTCTGTCACTC 81
Db      20 CCTGACGCGCTCTGTCACTC 1

RESULT 321
US-09-754-167-53/c
/ Sequence 53, Application US/09754167
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Jacqueline Wyatt
/ TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
/ FILE REFERENCE: RTS-0140
/ CURRENT APPLICATION NUMBER: US/09/754,167
/ CURRENT FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 87
/ SEQ ID NO 53
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-53

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1246 TCCAAACGCGAGCGATTCCT 1265
Db      20 TCCAAATGCGAGCGATTCCT 1

RESULT 320
US-10-145-493B-40/c
/ Sequence 40, Application US/10145493B
/ GENERAL INFORMATION:
/ APPLICANT: Besterman, Jeffrey
/ APPLICANT: MacLeod, Robert
/ APPLICANT: Siders, William
/ TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
/ FILE REFERENCE: MET-015DV
/ CURRENT APPLICATION NUMBER: US/10/145,493B
/ CURRENT FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 09/420,692
/ PRIOR FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: US 60/104,804
/ PRIOR FILING DATE: 1998-10-19
/ NUMBER OF SEQ ID NOS: 90
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 40
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
US-10-145-493B-40

Query Match      1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      62 CCTGACGCGCTCTGTCACTC 81
Db      20 CCTGACGCGCTCTGTCACTC 1

RESULT 321
```

```
US-10-145-493B-42/c
; Sequence 42, Application US/10145493B
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-42
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1531 GGGTCAGGAGGAGGCGCAAG 1550
DB 20 GGGTCAGGAGGAGGCGCAAG 1

RESULT 322
US-10-154-659-12/c
; Sequence 12, Application US/10154659
; GENERAL INFORMATION:
; APPLICANT: Buxton, Francis P.
; APPLICANT: Cohen, Dalia
; APPLICANT: Fischer, Denise D
; APPLICANT: Wang, Shaowen
; TITLE OF INVENTION: Antisense oligonucleotides directed to
; FILE OF INVENTION: genes regulated by trapoxin-induced HDAC inhibition
; FILE REFERENCE: 4-32017A
; CURRENT APPLICATION NUMBER: US/10/154,659
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/293,090
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/344,416
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/370,332
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense oligonucleotide
; NAME/KEY: modified base
; LOCATION: (6)...(13)
; OTHER INFORMATION: 2'-H, phosphorothioate
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 2
; OTHER INFORMATION: 2' methoxyethyl 5-methyl cytidine
; NAME/KEY: modified base
; LOCATION: 1,3-5,14-18
; OTHER INFORMATION: 2'-O-methoxyethyl
US-10-154-659-12
```

```
Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 AACATGTCGAGTACAGC 374
DB 18 AACATGTCGAGTACAGC 1

RESULT 323
US-10-751-736-43856/c
; Sequence 43856, Application US/10751736
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43856
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-751-736-43856
```

```
Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 129 ACCCGAGGAGAACTCTGTAC 149
DB 21 AACCGAGGAGAACTCTGTAC 1
```

```
RESULT 324
US-10-266-090-51356/c
; Sequence 51356, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: Goff, Stephen
; APPLICANT: Bonan, Caroline
; APPLICANT: Colbert, Michelle
; APPLICANT: Wang, Rong-Lin
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51356
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-51356
```

```
Query Match 1.1%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1380 GAAGAGGAGGAGGGGG 1398
Db 20 GAAGAGGAGAGAGGGGG 2

RESULT 325
PCT-US98-04571A-122
; Sequence 122, Application PC/TUS9804571A
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: GENETIC COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 686
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/04571A
; FILING DATE: 03-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,125
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: 08/813,159
; FILING DATE: 07-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-029002PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US98-04571A-122

Query Match 1.1%; Score 17; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1480 AAGGAATCACCAGAGGA 1498
Db 3 AAGGAACCCGAGAGGA 21

RESULT 326
US-08-813-159-122
; Sequence 122, Application US/08813159
; GENERAL INFORMATION:
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Chee, Mark
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Berno, Anthony
; TITLE OF INVENTION: Genetic Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,159
FILING DATE: 03-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-029001US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-813-159-122

Query Match 1.1%; Score 17; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1480 AAGGAATCACCAGAGGA 1498
Db 3 AAGGAACCCGAGAGGA 21

RESULT 327
PCT-US02-29148-65/c
; Sequence 65, Application PC/TUS0229148
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0413
; CURRENT APPLICATION NUMBER: PCT/US02/29148
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/953,318
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-29148-65

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCTGCACCATGCAA 537
Db 20 TGGGAGCCTGCACCAAGCAA 1

RESULT 328
US-09-514-000-14731

```

; Sequence 14731, Application US/09514000
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)B
; CURRENT APPLICATION NUMBER: US/09/514,000
; CURRENT FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 15034
; SEQ ID NO 14731
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-514-000-14731

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 958 ACTGTGTGGAATTTGTCAG 977
Db 1 AGGGTGTGGAATTTGTCAG 20

RESULT 329
US-09-553-318-65/c
; Sequence 65, Application US/09953318
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/09/953,318
; CURRENT FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-318-65

Query Match      1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCGCTGCACATGCAA 537
Db 20 TGGGAGCGCTGCACCAAGCAA 1

RESULT 330
US-10-446-373-65/c
; Sequence 65, Application US/10446373
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
; FILE REFERENCE: RTS-0232
; CURRENT APPLICATION NUMBER: US/10/446,373
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/953,318
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

```

US-10-446-373-65

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCGCTGCACATGCAA 537
Db 20 TGGGAGCGCTGCACCAAGCAA 1

RESULT 331
US-10-310-188-35269
; Sequence 35269, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35269
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-35269

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1446 GAGGATGAAAAGAGAGAGA 1465
Db 1 GAGGATGAAAAGAGAGAGA 20

RESULT 332
US-10-751-736-12071
; Sequence 12071, Application US/10751736
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON CANCER
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12071
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-12071

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1533 CTCAGGAGGAGGCCCAAGTT 1552
Db 2 GUCAAGGAGAGGCCCAAUU 21

RESULT 333
US-10-751-736-28225
; Sequence 28225, Application US/10751736

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28225
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-28225

Query Match      1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 AAGAACTCTCCAACTTCAA 1423
Db 2 AAGAACTCTCCAACTTCAA 21

RESULT 334
US-10-751-736-28228
; Sequence 28228, Application US/10751736
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28228
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-28228

Query Match      1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1404 AAGAACTCTCCAACTTCAA 1423
Db 1 AAGAACTCTCCAACTTCAA 20

RESULT 335
PCT-US02-38147-198/c
; Sequence 198, Application PC/TUS0238147
; GENERAL INFORMATION:
; APPLICANT: Cell-Matrix, Inc.
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; APPLICANT: Broek, Daniel
; APPLICANT: Brooks, Peter C.
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods

; FILE REFERENCE: P-IX 5082
; CURRENT APPLICATION NUMBER: US/10/011,250
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence

PCT-US02-38147-198
; FILE REFERENCE: P-IX 5532
; CURRENT APPLICATION NUMBER: PCT/US02/38147
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/995,529
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
PCT-US02-38147-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCCA 1469
Db 17 AAAAAGAGAAAGAYCCA 1

RESULT 336
US-09-995-529-198/c
; Sequence 198, Application US/09995529
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-995-529-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCCA 1469
Db 17 AAAAAGAGAAAGAYCCA 1

RESULT 337
US-10-011-250-198/c
; Sequence 198, Application US/10011250
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 5082
; CURRENT APPLICATION NUMBER: US/10/011,250
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; FEATURE:
; OTHER INFORMATION: Primer
US-10-011-250-198

Query Match      1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAAGACCA 1469
Db 17 AAAAAGAGAAAGAYCCA 1

RESULT 338
US-10-310-188-43026
; Sequence 43026, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 43026
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-43026

Query Match      1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1465 ACCAGGAGGAGGAAG 1482
Db 1 ACCAGTGGAGAGGAAG 18

RESULT 339
PCT-US03-35845-27/c
; Sequence 27, Application PC/TUS0335845
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE 11
; FILE REFERENCE: ISI0008-500WO (HTS-0090WO)
; CURRENT APPLICATION NUMBER: PCT/US03/35845
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 10/293,863
; PRIOR FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US03-35845-27

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1512 GAGAAGCCAGAGCCAAA 1529
Db 19 GTGAAGCCAGAGCCAAA 2

RESULT 340
PCT-US03-35845-61

```

```

; Sequence 61, Application PC/TUS0335845
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE 11
; FILE REFERENCE: ISI0008-500WO (HTS-0090WO)
; CURRENT APPLICATION NUMBER: PCT/US03/35845
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 10/293,863
; PRIOR FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 81
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
PCT-US03-35845-61

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1512 GAGAAGCCAGAGCCAAA 1529
Db 2 GTGAAGCCAGAGCCAAA 19

RESULT 341
US-08-465-866B-13/c
; Sequence 13, Application US/08465866B
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; TITLE OF INVENTION: Gapped Oligonucleotides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,866B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 244,993
; FILING DATE: 21-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-465-866B-13

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1507 AGGAGGAGAGCCAGAG 1524
| | | | | | | | | | | | | | | | | | | | | |
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 342

US-08-756-806-27/c
; Sequence 27, Application US/08756806
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P. and Boggs, Russell T.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,806
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0200
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-756-806-27

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
| | | | | | | | | | | | | | | | | | | | | |
Db 19 AGGAGGAGAGCCAGAG 2

US-08-756-806-27/c
; Sequence 27, Application US/08756806
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia

RESULT 343

US-09-996-263-13/c
; Sequence 13, Application US/09996263
; GENERAL INFORMATION:
; APPLICANT: Andrew Kawasaki

; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
| | | | | | | | | | | | | | | | | | | | | |
Db 19 AGGAGGAGAGCCAGAG 2

STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/996,263
FILING DATE: 28-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,973
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucchi
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-996-263-13

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
| | | | | | | | | | | | | | | | | | | | | |
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 344

US-10-057-550-28/c
; Sequence 28, Application US/10057550
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/057,550
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/506,073
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550-28

```
Query Match          1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
    |||||
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 345
US-10-057-550A-27/c
; Sequence 27, Application US/10057550A
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0625
; CURRENT APPLICATION NUMBER: US/10/057,550A
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-057-550A-27

Query Match          1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
    |||||
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 346
US-10-173-225B-27/c
; Sequence 27, Application US/10173225B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of raf Gene Expression
; FILE REFERENCE: ISPH-0665
; CURRENT APPLICATION NUMBER: US/10/173,225B
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 10/057,550
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 09/143,214
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: PCT/US98/13961
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: US 08/888,982
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US 08/756,806
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: PCT/US95/07111
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/250,856
; PRIOR FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 27
```

```
Query Match          1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
    |||||
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 347
US-10-266-090-45347/c
; Sequence 45347, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GORF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; FILE REFERENCE: NADII.058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45347
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-45347

Query Match          1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1293 GATGAGGAGAGGAGCAG 1310
    |||||
Db 20 GATGAGGAGAGGAGCAG 3

RESULT 348
US-10-293-863-27/c
; Sequence 27, Application US/10293863
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE 11
; FILE REFERENCE: HTS-0090
; CURRENT APPLICATION NUMBER: US/10/293,863
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-863-27

Query Match          1.0%; Score 16.4; DB 1; Length 20;
```



```

Best Local Similarity 94.4%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;

QY 1512 GAGAAGCCAGAGCCCAA 1529
Db 19 GTGAAGCCAGAGCCCAA 2

RESULT 349
US-10-293-863-61
; Sequence 61, Application US/10293863
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF MITOGEN-ACTIVATED PROTEIN KINASE KINASE 11 E
; FILE REFERENCE: HTS-0090
; CURRENT APPLICATION NUMBER: US/10/293,863
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
;
US-10-293-863-61

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;

QY 1512 GAGAAGCCAGAGCCCAA 1529
Db 2 GTGAAGCCAGAGCCCAA 19

RESULT 350
US-10-352-586-13/c
; Sequence 13, Application US/10352586
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; FILE REFERENCE: ISIS5137
; CURRENT APPLICATION NUMBER: US/10/352,586
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 09/389,283
; PRIOR FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-352-586-13

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1;

QY 1507 AGGAGGAGAGCCAGAG 1524
Db 19 AGGAGGAGAGCCAGAG 2

RESULT 351
US-09-426-753-24
; Sequence 24, Application US/09426753
; GENERAL INFORMATION:
; APPLICANT: Margolis, Russell
; APPLICANT: Ross, Christopher

```

```

; APPLICANT: Nisson, Paul
; APPLICANT: Li, Wu
; TITLE OF INVENTION: CCG repeats in cDNAs from human brain
; FILE REFERENCE: 01107.83651
; CURRENT APPLICATION NUMBER: US/09/426,753
; CURRENT FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: 60/105,885
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 09/426,753
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-426-753-24

Query Match 1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2;

QY 1292 CGATGAGGAGGAGCGAC 1310
Db 1 CGATGAGGAGGAGCGAC 19

RESULT 352
US-10-125-568-24
; Sequence 24, Application US/10125568
; GENERAL INFORMATION:
; APPLICANT: Margolis, Russell
; APPLICANT: Ross, Christopher
; APPLICANT: Nisson, Paul
; APPLICANT: Li, Wu
; TITLE OF INVENTION: CCG repeats in cDNAs from human brain
; FILE REFERENCE: 01107.83651
; CURRENT APPLICATION NUMBER: US/10/125,568
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/426,753
; PRIOR FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: 60/105,885
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 09/426,753
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-125-568-24

Query Match 1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2;

QY 1292 CGATGAGGAGGAGCGAC 1310
Db 1 CGATGAGGAGGAGCGAC 19

RESULT 353
US-10-310-188-38959
; Sequence 38959, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841

```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38959
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-38959

Query Match      1.0%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 TGAGAGGAGGAGGAGGGG 1397
Db 1 TGAGAGGAGGAGGAGGGG 19

RESULT 354
PCT-US02-25940-16869/c
; Sequence 3283, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 16869
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2032440)...(2032457)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 19728
PCT-US02-25940-16869

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTCGCT 1356
Db 17 TGACAAACGAATTCGCT 1

RESULT 355
US-09-546-745A-3283/c
; Sequence 3283, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3283
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-3283

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1417 ACTTCAAAAAGGCCAAG 1433
```

```
Db 17 ACTTCAAAAAGGCCAAG 1

RESULT 356
US-09-546-745A-3284/c
; Sequence 3284, Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
; FILE REFERENCE: 237/193
; CURRENT APPLICATION NUMBER: US/09/546,745A
; CURRENT FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 7043
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-745A-3284

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1415 CACTTCAAAAAGGCCA 1431
Db 17 CAACTTCAAAAAGGCCA 1

RESULT 357
US-10-227-563-16869/c
; Sequence 16869, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 16869
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2032440)...(2032457)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1972
US-10-227-563-16869

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTCGCT 1356
Db 17 TGACAAACGAATTCGCT 1

RESULT 358
US-10-367-892-16869/c
; Sequence 16869, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
```

```
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 16869
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2032440)...(2032457)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 19728
US-10-367-892-16869

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAAATTCCT 1356
Db 17 TGACAAAGAAATTCCT 1

RESULT 359
PCT-US00-00654-44/c
; Sequence 44, Application PC/TUS0000654
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTSP-0044
; CURRENT APPLICATION NUMBER: PCT/US00/00654
; CURRENT FILING DATE: 2000-01-11
; EARLIER APPLICATION NUMBER: US 09/255,912
; EARLIER FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US00-00654-44

Query Match      1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1557 TGAATGGACCTCTCCAG 1573
Db 18 TGAATGGACCTCTACAG 2

RESULT 360
US-09-913-684-44/c
; Sequence 44, Application US/09913684
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTSP-0160
; CURRENT APPLICATION NUMBER: US/09/913,684
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 09/255,912
; PRIOR FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-913-684-44

Query Match      1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1469 AGAGGAGAGAAAGGAA 1485
Db 17 AGAGGAGAGAAATGGAA 1

RESULT 362
PCT-US03-05044-34
; Sequence 34, Application PC/TUS0305044
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
; TITLE OF INVENTION: Growth Factor Receptor (IGF-IR) Gene Expression Using Short
; FILE REFERENCE: 400/108 (MEHB03-195)
; CURRENT APPLICATION NUMBER: PCT/US03/05044
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
US-10-349-143-5052

Query Match      1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1469 AGAGGAGAGAAAGGAA 1485
Db 17 AGAGGAGAGAAATGGAA 1

RESULT 362
PCT-US03-05044-34
; Sequence 34, Application PC/TUS0305044
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowira, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
; TITLE OF INVENTION: Growth Factor Receptor (IGF-IR) Gene Expression Using Short
; FILE REFERENCE: 400/108 (MEHB03-195)
; CURRENT APPLICATION NUMBER: PCT/US03/05044
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
US-10-349-143-5052
```

; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 604
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 34
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
PCT-US03-05044-34

Query Match 1.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 ACCAAGGAGGAGAGCC 1519
||| |||||
Db 2 ACCAUGGAGGAGAGCC 18

RESULT 363
PCT-US03-05044-311/c
; Sequence 311, Application PC/TUS0305044
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Chowika, Bharat
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Type 1 Insulin-like
; TITLE OF INVENTION: Growth Factor Receptor (IGF-1R) Gene Expression Using Short
; TITLE OF INVENTION: Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/108 (MBH03-195)
; CURRENT APPLICATION NUMBER: PCT/US03/05044
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 604
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
PCT-US03-05044-311

Query Match 1.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 ACCAAGGAGGAGAGCC 1519
||| |||||
Db 18 ACCATGGAGGAGAGCC 2

RESULT 364
US-10-310-188-16111
; Sequence 16111, Application US/10310188

; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16111
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-16111

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1571 CAGCTCTGGCTTCCT 1585
|||||
Db 2 CAGCTCTGGCTTCCT 16

RESULT 365
US-10-266-090-38180
; Sequence 38180, Application US/10266090
; GENERAL INFORMATION:
; APPLICANT: GOFF, STEPHEN
; APPLICANT: BONAN, CAROLINE
; APPLICANT: COLBERT, MICHELLE
; APPLICANT: WANG, RONG-LIN
; TITLE OF INVENTION: CEREAL TRINUCLEOTIDE SIMPLE SEQUENCE
; TITLE OF INVENTION: REPEAT MARKERS AND THEIR USES
; FILE REFERENCE: NADII 058C1
; CURRENT APPLICATION NUMBER: US/10/266,090
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 10/260,703
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/326,117
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 51812
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38180
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR PRIMER FOR SEQUENCE FROM ORYZA SATIVA
US-10-266-090-38180

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1296 GAGGACGAGGAGCAGC 1310
|||||
Db 4 GAGGACGAGGAGCAGC 18

RESULT 366
PCT-US00-06067-23
; Sequence 23, Application PC/TUS0006067
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16PC
; CURRENT APPLICATION NUMBER: PCT/US00/06067
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 09/264,908
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 09/265,992
; EARLIER FILING DATE: 1999-03-11

```
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
PCT-US00-06067-23

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCGCTGC 528
Db      1 ACTGGGCTGGGGGACTGC 18

RESULT 367
US-08-282-197B-14/c
; Sequence 14, Application US/08282197B
; GENERAL INFORMATION:
; APPLICANT: Brzezinski, Ryszard
; APPLICANT: Dery, Claude V
; TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A
; REFERENCE/DOCKET NUMBER: 1050.0410000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-282-197B-14

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      689 CATGACTGTGTCCTTCA 706
Db      18 CATGGCTGTGCCCTTCA 1

RESULT 368
US-09-159-254-22
; Sequence 22, Application US/09159254
```

```
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: Cytokine receptor zalphall
; FILE REFERENCE: 98-55X
; CURRENT APPLICATION NUMBER: US/09/159,254
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-159-254-22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCGCTGC 528
Db      1 ACTGGGCTGGGGGACTGC 18

RESULT 369
US-09-264-908-22
; Sequence 22, Application US/09264908
; GENERAL INFORMATION:
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Xu, Wen-feng
; APPLICANT: Grant, Francis J.
; APPLICANT: Foster, Donald C.
; APPLICANT: Kuijper, Joseph L.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16X
; CURRENT APPLICATION NUMBER: US/09/264,908
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-264-908-22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      511 ATTGGGCTGGGGCGCTGC 528
Db      1 ACTGGGCTGGGGGACTGC 18

RESULT 370
US-09-264-908-39
; Sequence 39, Application US/09264908
; GENERAL INFORMATION:
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
```

```
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Xu, Wen-feng
; APPLICANT: Grant, Francis J.
; APPLICANT: Foster, Donald C.
; APPLICANT: Kuijper, Joseph L.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16X
; CURRENT APPLICATION NUMBER: US/09/264,908
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-264-908-39
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGTC 528
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 371

```
US-09-265-117-22
; Sequence 22, Application US/09265117
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHAL1
; FILE REFERENCE: 98-55X2
; CURRENT APPLICATION NUMBER: US/09/265,117
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-265-117-22
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGTC 528
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 372

```
US-09-265-117-39
; Sequence 22, Application US/09265117
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHAL1
; FILE REFERENCE: 98-55X2
; CURRENT APPLICATION NUMBER: US/09/265,117
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 49
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-265-117-39
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGTC 528
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 373

```
US-09-265-992-23
; Sequence 23, Application US/09265992
; GENERAL INFORMATION:
; APPLICANT: Parrish, Julia E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Xu, Wen-feng
; APPLICANT: Grant, Francis J.
; APPLICANT: Foster, Donald C.
; APPLICANT: Kuijper, Joseph L.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16X2
; CURRENT APPLICATION NUMBER: US/09/265,992
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-265-992-23
```

```
Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      511 ATTGGGCTGGGGGCTGTC 528
Db       1 ACTGGGCTGGGGGACTGC 18
```

RESULT 374

```
US-09-347-930-22
; Sequence 22, Application US/09347930
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Raymond, Fenella C.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHAL1
; FILE REFERENCE: 98-55X3
; CURRENT APPLICATION NUMBER: US/09/347,930
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-347-930-22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
    |||||
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 375
US-09-347-930-39
; Sequence 39, Application US/09347930
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Parrish, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Raymond, Fenella C.
; APPLICANT: Hammond, Angela K.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55X3
; CURRENT APPLICATION NUMBER: US/09/347,930
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-347-930-39

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
    |||||
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 376
US-09-628-127-22
; Sequence 22, Application US/09628127
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/09/628,127
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
    |||||
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 377
US-09-628-127-39
; Sequence 39, Application US/09628127
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/09/628,127
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-09-628-127-39

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528
    |||||
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 378
US-10-243-072-22
; Sequence 22, Application US/10243072
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLH11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
```

```
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCTGC 528
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 379
US-10-243-072-39
; Sequence 39, Application US/10243072
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-243-072-39

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCTGC 528
Db 1 ACTGGGCTGGGGACTGC 18

RESULT 380
US-10-310-188-23157/c
; Sequence 23157, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
```

```
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23157
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-23157

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1495 AGGAGAAACCAAGGAGG 1512
Db 18 AGAAGAAACCAAGGAGG 1

RESULT 381
US-10-310-188-23178/c
; Sequence 23178, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23178
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-23178

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1495 AGGAGAAACCAAGGAGG 1512
Db 18 AGAAGAAACCAAGGAGG 1

RESULT 382
US-10-310-188-58290
; Sequence 58290, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58290
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-58290

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 TGAAGAGGAGGAGAGG 1396
Db 1 TGAAGAGGAGAGATCG 18

RESULT 383
US-10-310-188-58290
```



```
US-10-310-188-86028
; Sequence 86028, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 86028
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-86028

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1507 AGGAGGAGGAGCCAGAG 1524
Db 1 AGGAGGAGGAGACAGAG 18

RESULT 384
US-10-414-186-22
; Sequence 22, Application US/10414186
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGGCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 385
US-10-414-186-39
; Sequence 39, Application US/10414186
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-414-186-22

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGGCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 386
US-10-414-186-23
; Sequence 23, Application US/10659684
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZAPLHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-659-684-23

Query Match          0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGGCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18
```

```

Db      1 ACTGGGCTGGGGGACTGC 18

RESULT 387
US-10-715-998-22
; Sequence 22, Application US/10715998
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Novak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHALL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/715,998
; PRIOR FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19954
US-10-715-998-22

Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      511 ATTGGGCTGGGGGCTGC 528
      1 ACTGGGCTGGGGGACTGC 18

RESULT 389
US-08-563-105-3/c
; Sequence 3, Application US/08563105
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Economides, Aris
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: HETEROMERIC RECEPTORS AND METHODS FOR
; TITLE OF INVENTION: THEIR PRODUCTION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/563,105
; FILING DATE: 27-NOV-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,715
; FILING DATE: 14-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/140,222
; FILING DATE: 20-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
US-08-563-105-3

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      642 CACCATGGTGACGCG 657
      16 CACCATGGTGCGCGCG 1

RESULT 390
US-09-177-009-3/c
; Sequence 3, Application US/09177009
; GENERAL INFORMATION:

```

APPLICANT: Stahl, Neil
APPLICANT: Economidis, Aris
APPLICANT: Vancopoulos, George D.
TITLE OF INVENTION: HETEROMERIC RECEPTORS AND METHODS FOR
TITLE OF INVENTION: THEIR PRODUCTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,009
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/563,105
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: US 60/006,715
FILING DATE: 14-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/140,222
FILING DATE: 20-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-09-177-009-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 642 CACCATGGTGACGGCG 657

Db 16 CACCATGGTGCGGCG 1

RESULT 391
US-09-708-690-5827
Sequence 5827, Application US/09708690
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-L (400/002)
CURRENT APPLICATION NUMBER: US/09/708,690
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08

PRIOR APPLICATION NUMBER: US 09/371,772
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 09/685,664
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 20828
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5827
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-09-708-690-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 517 CTGGGGCCTGCACCA 532

Db 1 CUGGGAGCCUGACCA 16

RESULT 392
US-09-787-835-3/c
Sequence 3, Application US/09787835
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/09/787,835
CURRENT FILING DATE: 2002-12-12
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Kozak sequence
US-09-787-835-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 642 CACCATGGTGACGGCG 657

Db 16 CACCATGGTGCGGCG 1

RESULT 393
US-09-870-161-5827
Sequence 5827, Application US/09870161
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00-876-M (400/026)
CURRENT APPLICATION NUMBER: US/09/870,161
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 20821
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5827

```

; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-870-161-5827

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACCA 532
Db 1 CUGGGAGCCUGCACCA 16

RESULT 394
US-09-935-868-3/c
; Sequence 5827, Application US/09935868
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935.968
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-09-935-868-3

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
Db 16 CACCATGGTGACGGCG 1

RESULT 395
US-10-138-674-5827
; Sequence 5827, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5827

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACCA 532
Db 1 CUGGGAGCCUGCACCA 16

```

```

RESULT 396
US-10-138-674A-5827
; Sequence 5827, Application US/10138674A
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674A
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20826
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5827
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674A-5827

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACCA 532
Db 1 CUGGGAGCCUGCACCA 16

RESULT 397
US-10-282-162-3/c
; Sequence 3, Application US/10282162
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kozak sequence
US-10-282-162-3

Query Match      0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGGTGACGGCG 657
Db 16 CACCATGGTGACGGCG 1

RESULT 398
US-10-287-035-3/c
; Sequence 3, Application US/10287035
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Vancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING

```

FILE REFERENCE: REG 203DA
CURRENT APPLICATION NUMBER: US/10/287,035
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Kozak sequence
US-10-287-035-3

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 642 CACATGGTGACCGCG 657
Db 16 CACATGGTGCGCGC 1

RESULT 399
US-10-287-949A-5827
Sequence 5827, Application US/10287949A
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MEH800-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5827
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-10-287-949A-5827

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 517 CTGGGGCCTGCACCA 532
Db 1 CUGGAGCCGACCA 16

RESULT 400
US-10-310-188-39096
Sequence 39096, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19

NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 39096
LENGTH: 16
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-39096

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1383 GAGGAGGGGAGAGGGGG 1398
Db 1 GAGGAGGGGAGAGGGGG 16

RESULT 401
PCT-US01-29656-779/c
Sequence 779, Application PC/TUS0129656
GENERAL INFORMATION:
APPLICANT: ZHANG, Jian
APPLICANT: AECOMICA, INC.
TITLE OF INVENTION: HUMAN KIDNEY TUMOR OVEREXPRESSED MEMBRANE PROTEIN 1
FILE REFERENCE: AECOMICA-18 PCT
CURRENT APPLICATION NUMBER: PCT/US01/29656
CURRENT FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/315,676
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: GB 0024263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00659
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 2034
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 779
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-29656-779

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1247 CCAAAAGCAGCGGATT 1262
Db 17 CCAAAATGCAGCGGATT 2

```

RESULT 402
PCT-US01-29656-780/c
; Sequence 780, Application PC/TUS0129656
; GENERAL INFORMATION:
; APPLICANT: ZHANG, Jian
; APPLICANT: AEWOMICA, INC.
; TITLE OF INVENTION: HUMAN KIDNEY TUMOR OVEREXPRESSED MEMBRANE PROTEIN 1
; FILE REFERENCE: AEWOMICA-18 PCT
; CURRENT APPLICATION NUMBER: PCT/US01/29656
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/315,676
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: GB 024263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 2034
; SOFTWARE: Aewomica Sequence Listing Engine
; SEQ ID NO 780
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-29656-780

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1247 CCAACGCGCGGATT 1262
Db 16 CCAATGCGCGGATT 1

RESULT 403
PCT-US02-17674-678
; Sequence 678, Application PC/TUS0217674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gild
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
; FILE REFERENCE: 400/047 (02-325)
; CURRENT APPLICATION NUMBER: PCT/US02/17674
; CURRENT FILING DATE: 2003-03-25

```

```

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 678
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
PCT-US02-17674-678

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGGCGCTGCACC 531
Db 2 GCUGGGAGCCUGCACC 17

RESULT 404
PCT-US02-25940-19155/c
; Sequence 19155, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 19155
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2327709)...(2327725)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 2245
PCT-US02-25940-19155

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATGCC 1355
Db 16 TGACAAAGAATGCC 1

RESULT 405
US-09-541-946-1695
; Sequence 1695, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altshuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipschutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE

```

```

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e-02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1237 CACCTGGGGTCCAAAC 1252
          |||||
Db      1 CAGCTGGGGTCCAAAC 16

RESULT 407
US-09-546-745A-3282/c
; Sequence 3282. Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules

```

```

Query Match          0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e-02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1237 CACCTGGGGTCCAAAC 1252
          |||||
Db      1 CAGCTGGGGTCCAAAC 16

RESULT 407
US-09-546-745A-3282/c
; Sequence 3282. Application US/09546745A
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Zwick, Michael
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, Jim
; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules

```



```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674A-7632

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGGCTGCACC 531
Db 2 GCUGGAGCCUGCACC 17

RESULT 419
US-10-227-563-19155/c
; Sequence 19155, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 19155
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; LOCATION: (2327709)...(2327725)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 22452
US-10-227-563-19155

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTGCC 1355
Db 16 TGACAAAGAATTGCC 1

RESULT 420
US-10-287-949A-4754
; Sequence 4754, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4754

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACC 532
Db 1 CUGGAGCCUGCACC 16
```

```

RESULT 421
US-10-287-949A-7632
; Sequence 7632, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7632
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7632

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGGCTGCACC 531
Db 2 GCUGGAGCCUGCACC 17

RESULT 422
US-10-310-188-18308
; Sequence 18308, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18308
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-18308

Query Match
Best Local Similarity 0.9%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1383 GAGGAGGAGGAGGGGG 1398
Db 2 GAGGAGGAGGAGGGAG 17

RESULT 423
US-10-367-892-19155/c
; Sequence 19155, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 19155
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
```

```
; FEATURE:
; LOCATION: (2327709)...(2327725)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 22452
US-10-367-892-19155

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1340 TGACAAACGAATTGCC 1355
Db 16 TGACAAAAGAAATGCC 1

RESULT 424
US-10-712-633-678
; Sequence 678, Application US/10712633
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: MHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712.633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 678
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-678

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.8e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 516 GCTGGGGCGCTGCACC 531
Db 2 GCUGGAGCCUGCACC 17

RESULT 425
US-10-723-361-971/c
; Sequence 971, Application US/10723361
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
```

```
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 971
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-971

Query Match      0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TTGGGCTGGGGCGCTG 527
Db 17 TTGGGCTTGGGGCGCTG 2

RESULT 426
US-10-723-361-972/c
; Sequence 972, Application US/10723361
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART P
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
```

```

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 972
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-972

```

Query Match	0.9%	Score 14.4;	DB 1;	Length 17;
Best Local Similarity	93.8%	Pred. No. 2.8e+02;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	512	TTGGGCTGGGGCCTG	527	
Db	16	TTGGGCTTGGGGCCTG	1	

RESULT 427
US-60-315-676-779/c
; Sequence 779, Application US/60315676
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN KIDNEY TUMOR OVEREXPRESSED MEMBRANE PROTEIN 1

```

, FILE REFERENCE: AEOMLICA-18
, CURRENT APPLICATION NUMBER: US/60/315,676
, CURRENT FILING DATE: 2001-08-28
, PRIOR APPLICATION NUMBER: GB 0024263.6
, PRIOR FILING DATE: 2000-10-04
, PRIOR APPLICATION NUMBER: US 60/236,359
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: PCT/US01/00666
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00667
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00664
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00669
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00665
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00668
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00663
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00662
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00661
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/864,781
, PRIOR FILING DATE: 2001-05-23
, NUMBER OF SEQ ID NOS: 2034
, SOFTWARE: Aecomica Sequence Listing Engine
, SEQ ID NO 779
, LENGTH: 17
, TYPE: DNA
, ORGANISM: Homo sapiens
, US-60-315-576-779

```

Query Match	0.9%	Score 14.4	DB 1	Length 17
Best Local Similarity	93.8%	Pred. NO. 2.8e+02		
Matches 15	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

Qy 1247 CCAAACGCAGGCGATT 1262
Db 17 CCAAATGCAGGCGATT 2

RESULT 428
US-60-315-676-780/c
; Sequence 780. Application US/60315676
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN KIDNEY TUMOR OVEREXPRESSED MEMBRANE PROTEIN 1
; FILE REFERENCE: A60MICA-18
; CURRENT APPLICATION NUMBER: US/60/315,676
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: GB 0034263.6

```

, PRIOR FILING DATE: 2000-10-04
, PRIOR APPLICATION NUMBER: US 60/236,359
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: PCT/US01/00666
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00667
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00664
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00669
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00665
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00668
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00663
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00662
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00661
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/00670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/864,761
, PRIOR FILING DATE: 2001-05-23
, NUMBER OF SEQ ID NOS: 2034
, SOFTWARE: Aecomica Sequence Listing Engine
, SEQ ID NO 780
, LENGTH: 17
, TYPE: DNA
, ORGANISM: Homo sapiens
, US-60-315-676-780

```

Query Match	0.9%	Score 14.4;	DB 1;	Length 17;
Best Local Similarity	93.8%;	Pred. No. 2.8e+02;		
Matches	15: Conservative	0: Mismatches	1: Indels	0: Gaps

Qy 1247 CCAAACGAGGCGATT 1262
Dy 16 CCAAATGCAGGCGATT 1

```

RESULT 429
US-60-339-764-2348/c
; Sequence 2348, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AECMICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 2348
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2348

```

Query Match 0.98; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2.8e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1501 AAACCAAGGAGGAGAA 1516
Db 17 AAACCAAGGAGGAGCA 2

RESULT 430
US-60-339-764-2349/c
Sequence 2349, Application US/60339764
GENERAL INFORMATION:
APPLICANT: Guo, Jinjiao
TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
FILE REFERENCE: AEMICA-31
CURRENT APPLICATION NUMBER: US/60/339,764
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 3310
SOFTWARE: Aemica Sequence Listing Engine
SEQ ID NO 2349
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-60-339-764-2349

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAA 1516
Db 16 AAACCAAGGAGGAGCA 1

RESULT 431
US-08-406-779-74/c
Sequence 74, Application US/08406779
GENERAL INFORMATION:
APPLICANT: AHRWEILER, PATRICIA
TITLE OF INVENTION: ALTERED AFFINITY POLYPEPTIDES OF METAL
TITLE OF INVENTION: CHELATE BINDING ANTIBODIES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,779
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/975,230
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-HY 9411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid

STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..18
US-08-406-779-74

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 611 CCAGAGGTTGCTGAC 626
Db 18 CCAGAGGTTGCTGAC 3

RESULT 432
US-08-803-305-4/c
Sequence 4, Application US/08803305
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmsberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Fartah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,305
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
IMMEDIATE SOURCE:
CLONE: ZC11107
US-08-803-305-4

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGCCAG 1470

```
Db      17 AAAGAGAAACCCAG 2

RESULT 433
US-08-803-305A-4/c
; Sequence 4, Application US/08803305A
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,305A
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 98-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; IMMEDIATE SOURCE:
; CLONE: ZC11107
US-08-803-305A-4

Query Match      0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1455 AAAGAGAAACCCAG 1470
Db      17 AAAGAGAAACCCAG 2

RESULT 434
US-09-275-712-4/c
; Sequence 4, Application US/09275712
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: Class II Cytokine Receptor-7

FILE REFERENCE: 96-24D1
; CURRENT APPLICATION NUMBER: US/09/275,712
; CURRENT FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 08/943,087
; EARLIER FILING DATE: 1997-10-02
; EARLIER APPLICATION NUMBER: 08/803,305
; EARLIER FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-275-712-4

Query Match      0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1455 AAAGAGAAACCCAG 1470
Db      17 AAAGAGAAACCCAG 2

RESULT 435
US-09-463-075A-165
; Sequence 165, Application US/09463075A
; GENERAL INFORMATION:
; APPLICANT: COHEN, Daniel
; BLUMENFELD, Marta
; TCHOUMAKOV, Ilia
; TITLE OF INVENTION: Biallelic markers for use in
; constructing a high density disequilibrium map of
; the human genome.
; NUMBER OF SEQUENCES: 336
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 550 West C Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/463,075A
; FILING DATE: 14-Jan-2000
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: downstream amplification primer for SEQ ID15, SEQ ID65
; LOCATION: 1..18
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-463-075A-165

Query Match      0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1457 AGAGAAAGACCCAG 1472
Db      1 AGAGAAAGACCCAG 16
```

```
RESULT 436
US-10-269-557-46
; Sequence 46, Application US/10269557
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/10/269,557
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/207,388
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Used to clone Neisseria meningitidis Hsp70
; OTHER INFORMATION: Gene and to construct Neisseria meningitidis Hsp70
; OTHER INFORMATION: expression vectors
US-10-269-557-46
Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 AAGCCAATGCTGAGGA 298
Db 2 AAGCCAATGCCGAGGA 17

RESULT 437
US-10-303-778-7630/c
; Sequence 7630, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7630
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-7630
Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1380 GAAGAGGAGGAGGAGG 1395
Db 18 GAAGAGGAGTGAGAGG 3

RESULT 438
US-10-303-778-8260
; Sequence 8260, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
; TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8260
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-8260
Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGG 1400
Db 3 GGAGGGAGAGGGGGG 18

RESULT 439
US-10-310-188-14763
; Sequence 14763, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14763
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-14763
Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGG 1400
Db 3 GGAGGGAGAGGGGGG 18

RESULT 440
US-10-310-188-18291
; Sequence 18291, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18291
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-18291
Query Match          0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1383 GAGGAGGAGAGGGGG 1398
Db 3 GAGGAGGAGAGGGAG 18

RESULT 441
US-10-310-188-29093/c
; Sequence 29093, Application US/10310188
```

```

QY 1470 GAGGAGGAAGGAA 1485
   |||||||
Db 2 GAGGAGGACGAGGAA 17

RESULT 444
US-10-310-188-86059
; Sequence 86059, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: Rosetademonics
; TITLE OF INVENTION: BIOINTELLIGENTLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENI
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86059
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-86059

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1506 AAGGAGGAGGAGCCAG 1521
   |||||||
Db 3 AAGGAGGAGGAGGCGAG 18

RESULT 445
US-10-349-143-4102
; Sequence 4102, Application US/10349143
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4102
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13273 for SEQ 168,
US-10-349-143-4102

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 ATGTCTGGGTCTCTG 16
Db 1 ATGTCTGGGTCTCTG 16

RESULT 446

```


Sequence 9179, Application US/10349143
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Iliya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 9179
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: downstream amplification primer 99-2275 for SEQ 1314, in complete
US-10-349-143-9179
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1457 AGAGAAAGACCAG 1472
DB 1 AGAGAAAGACCAG 16
RESULT 447
US-10-367-438-165
Sequence 165, Application US/10367438
GENERAL INFORMATION:
APPLICANT: COHEN, Daniel
APPLICANT: BLUMENFELD, Marta
APPLICANT: TCHOUMAKOV, Iliya
TITLE OF INVENTION: Biallelic markers for use in
constructing a high density disequilibrium map of
the human genome.
NUMBER OF SEQUENCES: 336
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 550 West C Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/367,438
FILING DATE: 14-Feb-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/463,075A
FILING DATE: 14-Jan-2000
INFORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: DNA

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: downstream amplification primer for SEQ ID15, SEQ ID65
LOCATION: 1..18
SEQUENCE DESCRIPTION: SEQ ID NO: 165;
US-10-367-438-165
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1457 AGAGAAAGACCAG 1472
DB 1 AGAGAAAGACCAG 16
RESULT 448
US-10-636-716-4/c
Sequence 4, Application US/10636716
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: CYTOKINE RECEPTOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/636,716
FILING DATE: 07-AUG-2003
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,087
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
IMMEDIATE SOURCE:
CLONE: 2C11107
US-10-636-716-4
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1455 AAAGAGAAAGACCCAG 1470
DB 17 AAAGAGAAACACCCAG 2

RESULT 449

US-60-082-614-2026
; Sequence 2026, Application US/60082614
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a
; TITLE OF INVENTION: high density disequilibrium
; NUMBER OF SEQUENCES: 2730
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/082,614
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.020PR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 2026:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: downstream amplification primer for SEQ ID67 and SEQ ID720
; LOCATION: 1..18
US-60-082-614-2026

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAG 1472
DB 1 AGAGAAAGACCCAG 16

Search completed: June 24, 2004, 10:20:06
Job time : 10 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	27	1.7	27	1	AB283012	Toxicologically re
2	26	1.6	26	1	AAA55804	Human histone deac
3	26	1.6	26	1	AAH43114	Antisense oligo, t
4	26	1.6	26	1	AAC89934	Human HDAC-1/HDAC-
5	26	1.6	26	1	AAC89943	Human HDAC-1/HDAC-
6	25.4	1.6	27	1	AB283014	Toxicologically re
7	24.4	1.5	26	1	AAC899541	Human HDAC-1/HDAC-
8	24.4	1.5	26	1	AAC899533	Human HDAC-1/HDAC-
9	24.4	1.5	26	1	AAC899532	Human HDAC-1/HDAC-
10	24.4	1.5	26	1	AAC899542	Human HDAC-1/HDAC-
11	23.4	1.5	26	1	AAA55837	Histone deacetylase
12	23.4	1.5	26	1	AAA55838	Histone deacetylase
13	23	1.4	23	1	AAA55802	Human histone deac
14	23	1.4	23	1	AAH43112	Antisense oligo, t
15	22.8	1.4	26	1	AAA55810	Human histone deac
16	22.8	1.4	26	1	AAH43120	Antisense oligo, t
17	22.8	1.4	26	1	AAC899935	Human HDAC-1/HDAC-
18	22.8	1.4	26	1	AAC899544	Human histone deac
19	22	1.4	22	1	AAA55803	Antisense oligo, t
20	22	1.4	22	1	AAH43113	Antisense oligo, t
21	21.4	1.3	23	1	AAA55808	Human histone deac
22	21.4	1.3	23	1	AAH43118	Antisense oligo, t
23	20.4	1.3	22	1	AAA55809	Human histone deac
24	20.4	1.3	22	1	AAH43119	Antisense oligo, t
25	20	1.2	20	1	AAA55793	Human histone deac
26	20	1.2	20	1	AAA55792	Human histone deac
27	20	1.2	20	1	AAA55794	Human histone deac
28	20	1.2	20	1	AAA55800	Human histone deac
29	20	1.2	20	1	AAA55795	Human histone deac
30	20	1.2	20	1	AAA55796	Human histone deac
31	20	1.2	20	1	AAA55801	Human histone deac
32	20	1.2	20	1	AAA55798	Human histone deac
33	20	1.2	20	1	AAH43108	Antisense oligo, t

C 107	18.4	1.1	20	1	AAH43107	Antisense oligo, t	180	13.8	0.9	17	1	ABV79344	Human HTPL scannin
C 108	18.4	1.1	20	1	AAH43109	Antisense oligo, t	181	13.8	0.9	17	1	ABV79345	Human HTPL scannin
C 109	18.4	1.1	20	1	AAD40902	Human HDAL antisense	182	13.8	0.9	17	1	ABV79343	Human ERG hammerhe
C 110	18.4	1.1	20	1	AAD40927	Human HDAL antisense	183	13.8	0.9	17	1	ABK18013	Human ERG hammerhe
C 111	17	1.1	17	1	ABT39526	Tumour suppression	184	13.8	0.9	17	1	ABK18165	Human ERG hammerhe
C 112	17	1.1	17	1	ABT39292	Tumour suppression	185	13.8	0.9	17	1	ABN95838	Related to Bombyx
C 113	17	1.1	21	1	AAV67421	Nucleotide fragmen	C 186	13.8	0.9	17	1	ABL31482	Human HLA genotyPi
C 114	16.8	1.0	20	1	ABQ3091	Human oligonucleot	C 187	13.8	0.9	17	1	ABK55737	Human CLCA1 gene e
C 115	16.8	1.0	20	1	ABZ32578	T. tauschii/wheat	C 188	13.8	0.9	17	1	ABT21381	Multiplex group PC
C 116	16.8	1.0	20	1	ACC36770	Human oligonucleot	189	13.8	0.9	17	1	ABZ65102	Human HER2 DNazyme
C 117	16.8	1.0	20	1	ACC44266	Human VEGFR-1 chim	190	13.8	0.9	17	1	ABZ65104	Human H-Ras DNazyme
C 118	16.6	1.0	20	1	ADD94313	5' primer to ampli	191	13.8	0.9	17	1	ABZ61695	Human H-Ras DNazyme
C 119	16.4	1.0	17	1	AAT27507	Mouse HUI77/HUIV26	192	13.8	0.9	17	1	ACD62482	HCV minus strand D
C 120	16.4	1.0	20	1	AAZ35151	Human C-raf kinase	C 193	13.8	0.9	17	1	ACD60187	HCV DNazyme subetr
C 121	16.4	1.0	20	1	AAZ35151	Chimeric 2'-O-meth	194	13.8	0.9	17	1	ACD60187	HCV DNazyme subetr
C 122	16.4	1.0	20	1	AAT59728	Human raf inhibito	C 195	13.8	0.9	17	1	ACD60187	HCV DNazyme subetr
C 123	16.4	1.0	20	1	AAT62157	Human C-raf and de	C 196	13.8	0.9	17	1	ACD62411	HCV minus strand D
C 124	16.4	1.0	20	1	AAZ115070	C-raf antisense ch	C 197	13.8	0.9	17	1	ACD51143	HCV hammerhead rib
C 125	16.4	1.0	20	1	AAZ11537	Human C-raf kinase	C 198	13.8	0.9	17	1	ACD60202	HCV DNazyme subetr
C 126	16.4	1.0	20	1	AAZ10296	Chimeric antisense	C 199	13.8	0.9	17	1	ACC63240	Murine oligonucleo
C 127	16.4	1.0	20	1	AAZ48166	Oligonucleotide us	C 200	13.8	0.9	17	1	ACC63240	Murine oligonucleo
C 128	16.4	1.0	20	1	AAZ48166	C-raf chimeric pho	C 201	13.8	0.9	17	1	ADB42595	Tumour suppression
C 129	16.4	1.0	20	1	AAZ48166	Human C-raf kinase	C 202	13.8	0.9	17	1	ADB42595	Tumour suppression
C 130	16.4	1.0	20	1	AAZ48166	Human C-raf kinase	C 203	13.8	0.9	17	1	ADB42595	Tumour suppression
C 131	16.4	1.0	20	1	ACA42099	Antisense oligonuc	C 204	13.8	0.9	17	1	ADB42595	Tumour suppression
C 132	16.4	1.0	20	1	ACA61359	Human C-raf mRNA a	C 205	13.8	0.9	17	1	ADB42595	Tumour suppression
C 133	16.4	1.0	20	1	ADD44696	Hammerhead ribozym	C 206	13.8	0.9	17	1	ADB42595	Tumour suppression
C 134	16.4	1.0	20	1	AAZ03299	Hammerhead ribozym	C 207	13.8	0.9	17	1	ADB42595	Tumour suppression
C 135	16.4	1.0	20	1	AAZ03299	Hammerhead ribozym	C 208	13.8	0.9	17	1	ADB42595	Tumour suppression
C 136	16.4	1.0	20	1	AAZ03299	Hammerhead ribozym	C 209	13.8	0.9	17	1	ADB42595	Tumour suppression
C 137	15	0.9	18	1	AAZ03299	Hammerhead ribozym	C 210	13.8	0.9	17	1	ADB42595	Tumour suppression
C 138	14.8	0.9	18	1	AAZ03299	Hammerhead ribozym	C 211	13.8	0.9	17	1	ADB42595	Tumour suppression
C 139	14.8	0.9	18	1	AAZ03299	Hammerhead ribozym	C 212	13.8	0.9	17	1	ADB42595	Tumour suppression
C 140	14.8	0.9	18	1	AAZ03299	Hammerhead ribozym	C 213	13.8	0.9	17	1	ADB42595	Tumour suppression
C 141	14.8	0.9	18	1	AAZ03299	Hammerhead ribozym	C 214	13.8	0.9	17	1	ADB42595	Tumour suppression
C 142	14.8	0.9	18	1	AAZ03299	Hammerhead ribozym	C 215	13.8	0.9	17	1	ADB42595	Tumour suppression
C 143	14.8	0.9	18	1	AAZ03299	Hammerhead ribozym	C 216	13.8	0.9	17	1	ADB42595	Tumour suppression
C 144	14.8	0.9	18	1	AAZ03299	Hammerhead ribozym	C 217	13.8	0.9	17	1	ADB42595	Tumour suppression
C 145	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 218	13.8	0.9	17	1	ADB42595	Tumour suppression
C 146	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 219	13.8	0.9	17	1	ADB42595	Tumour suppression
C 147	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 220	13.8	0.9	17	1	ADB42595	Tumour suppression
C 148	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 221	13.8	0.9	17	1	ADB42595	Tumour suppression
C 149	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 222	13.8	0.9	17	1	ADB42595	Tumour suppression
C 150	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 223	13.8	0.9	17	1	ADB42595	Tumour suppression
C 151	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 224	13.8	0.9	17	1	ADB42595	Tumour suppression
C 152	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 225	13.8	0.9	17	1	ADB42595	Tumour suppression
C 153	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 226	13.8	0.9	17	1	ADB42595	Tumour suppression
C 154	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 227	13.8	0.9	17	1	ADB42595	Tumour suppression
C 155	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 228	13.8	0.9	17	1	ADB42595	Tumour suppression
C 156	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 229	13.8	0.9	17	1	ADB42595	Tumour suppression
C 157	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 230	13.8	0.9	17	1	ADB42595	Tumour suppression
C 158	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 231	13.8	0.9	17	1	ADB42595	Tumour suppression
C 159	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 232	13.8	0.9	17	1	ADB42595	Tumour suppression
C 160	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 233	13.8	0.9	17	1	ADB42595	Tumour suppression
C 161	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 234	13.8	0.9	17	1	ADB42595	Tumour suppression
C 162	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 235	13.8	0.9	17	1	ADB42595	Tumour suppression
C 163	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 236	13.8	0.9	17	1	ADB42595	Tumour suppression
C 164	14.4	0.9	17	1	AAZ03299	Hammerhead ribozym	C 237	13.8	0.9	17	1	ADB42595	Tumour suppression
C 165	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym	C 238	13.8	0.9	17	1	ADB42595	Tumour suppression
C 166	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym	C 239	13.8	0.9	17	1	ADB42595	Tumour suppression
C 167	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym	C 240	13.8	0.9	17	1	ADB42595	Tumour suppression
C 168	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym	C 241	13.8	0.9	17	1	ADB42595	Tumour suppression
C 169	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym	C 242	13.8	0.9	17	1	ADB42595	Tumour suppression
C 170	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym	C 243	13.8	0.9	17	1	ADB42595	Tumour suppression
C 171	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym	C 244	13.8	0.9	17	1	ADB42595	Tumour suppression
C 172	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							
C 173	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							
C 174	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							
C 175	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							
C 176	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							
C 177	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							
C 178	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							
C 179	13.8	0.9	17	1	AAZ03299	Hammerhead ribozym							

ALIGNMENTS

RESULT 1
 ABZ83012
 ID ABZ83012 standard; DNA; 27 BP.

```

XX AC ABZ83012;
XX DT
XX DE 14-MAY-2003 (first entry)
XX KW Toxicologically relevant human PCR primer #171.
XX KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003016500-A2.
XX PD 27-FEB-2003.
XX PF 16-AUG-2002; 2002WO-US026514.
XX PR 16-AUG-2001; 2001US-0313080P.
XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;
XX PI Alen P;
XX DR WPI; 2003-268322/26.
XX PT Determining a toxicological response to an agent, useful for screening of
XX PT drugs, comprises comparing the expression profile of one or more human
XX PT toxic response genes to a reference gene expression profile indicative of
XX PT toxicity.
XX PS Claim 1; Page 99; 455pp; English.
XX CC The present invention describes a method (M1) for determining a
XX CC toxicological response to an agent, which comprises comparing the
XX CC expression profile of one or more human toxic response genes to a
XX CC reference gene expression profile indicative of toxicity, and so
XX CC determining the presence of a toxic response to the agent. Also
XX CC described: (1) an array comprising one or more polynucleotides selected
XX CC from the genes corresponding to the partial sequences given in ABZ82842
XX CC to ABZ8784, or their fragments of at least 20 nucleotides, or homologues
XX CC ; and (2) determining if a gene putatively identified to be a toxic
XX CC response gene plays a role on toxic response pathways by determining the
XX CC expression profile of the gene after exposure of cells or a human subject
XX CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
XX CC exposing cells to an agent or isolating cells from a human subject who
XX CC was exposed to an agent; (b) obtaining the test gene expression profile
XX CC for a putatively identified toxic response gene after exposure to a known
XX CC toxic pharmaceutical or industrial agent; and (c) comparing the test
XX CC profile to the expression profile of a gene with a similar function or
XX CC comparing the test profile to the expression profile of that gene after
XX CC exposure to other known toxic compounds. The methods are useful for
XX CC predicting and determining toxicological responses on a cellular, organ
XX CC or system level. The arrays comprising the human genes are useful for
XX CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX SQ Sequence 27 BP; 7 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 1.7%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1047 ACATATGAGACAGCTGTGGCCCTGGAT 1073
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ACATATGAGACAGCTGTGGCCCTGGAT 27
| | | | | | | | | | | | | | | | | | | | | |
RESULT 2
AAAS5804/c
ID AAAS5804 standard; DNA; 26 BP.
XX AAAS5804;

```

```

XX DT
XX DE 01-SEP-2000 (first entry)
XX KW Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:47.
XX KW Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
XX KW modulation; inhibition; gene expression; combination therapy; p16;
XX KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX KW antiinflammatory; inflammation; asthma; ss.
XX OS Homo sapiens.
XX PN WO2000023112-A1.
XX PD 27-APR-2000.
XX PF 19-OCT-1999; 99WO-US024278.
XX PR 19-OCT-1998; 98US-0104804P.
XX PA (METH-) METHYLGENE INC.
XX PI Besterman JM, Macleod AR, Siders WM;
XX DR WPI; 2000-339532/29.
XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX PT with a synergistic amount of antisense oligonucleotide and protein
XX PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX PT of e.g. tumors.
XX PS Example 9; Page 29; 99pp; English.
XX CC The present invention describes a method for inhibiting the expression of
XX CC a gene in a cell comprising contacting the cell with an effective
XX CC synergistic amount of an antisense oligonucleotide which inhibits
XX CC expression of the gene, and an effective synergistic amount of a protein
XX CC effector of a product of the gene. Also described are: (1) a method for
XX CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX CC comprising an antisense oligonucleotide which inhibits expression of the
XX CC gene in operable association with a protein effector of the inhibitor of (3). The
XX CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX CC methods and compositions are useful as analytical tools for transgenic
XX CC studies and as therapeutic tools, e.g. as gene therapy tools for human
XX CC diseases including benign and malignant tumours, inflammation or asthma.
XX CC The methods, inhibitors and compositions of the invention that inhibit
XX CC expression or activity of a gene or gene product may be used to treat
XX CC patients having, or predisposed to developing, a disease responsive to
XX CC inhibition of the gene. These may also be used to activate silenced genes
XX CC to provide missing gene functions and improve a given condition.
XX CC Furthermore, the methods and compositions are useful as probes of the
XX CC physiological function of a gene product in an experimental cell culture
XX CC or animal system; and to evaluate the effect of inhibiting gene activity
XX CC or expression. AAAS5758 to AAAS5842 represent oligonucleotide sequences
XX CC which are used in the exemplification of the present invention
XX SQ Sequence 26 BP; 8 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GAATCCGATGACATCATATTTGCTG 236
| | | | | | | | | | | | | | | | | | | | | |
Db 26 GAATCCGATGACATCATATTTGCTG 1
| | | | | | | | | | | | | | | | | | | | | |
RESULT 3
AAH43114/c
ID AAH43114 standard; DNA; 26 BP.
XX AAH43114;

```

```
AC AAH43114;
XX
XX DT 19-SEP-2001 (first entry)
XX DE Antisense oligo, target HDAC-1 211-236.
XX KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
XX KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
XX KW fungal infections; ss.
XX OS Synthetic.
XX OS
XX OS
XX PN WO200138322-A1.
XX PD
XX PD 31-MAY-2001.
XX XX
XX XX 22-NOV-2000; 2000WO-IB001881.
XX XX
XX XX 23-NOV-1999; 99US-0167035P.
XX XX
XX XX (METH-) METHYLGENE INC.
XX XX
XX XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX XX
XX XX WPI; 2001-432601/46.
XX XX
XX XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX PT restenosis or fungal infections.
XX XX
XX XX Disclosure; Page 40; 147pp; English.
XX XX
XX XX The sequences given in AAH43102-14 are oligonucleotides which are
XX CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
XX CC may be used in combination with an inhibitor of histone deacetylase
XX CC enzyme function, to give an improved inhibitory effect, thereby reducing
XX CC the amount of inhibitor required to obtain a given inhibitory effect.
XX CC Compounds containing these oligonucleotides may be used to treat cell
XX CC proliferation conditions such as cancer, restenosis or psoriasis. They
XX CC can also be used to treat protozoal and fungal infections
XX XX
XX SQ Sequence 26 BP; 8 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 26; DB 1; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 6.6;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 211 GAATCCGCATGACTCATTAATTGCTG 236
XX DB 26 GAATCCGCATGACTCATTAATTGCTG 1
XX
XX RESULT 4
XX AAC89534/c
XX ID AAC89534 standard; DNA; 26 BP.
XX XX
XX AC AAC89534;
XX XX
XX XX Homo sapiens.
XX XX
XX XX WO200071703-A2.
XX XX
XX XX 30-NOV-2000.
XX XX
XX XX 03-MAY-2000; 2000WO-IB001252.
XX XX
XX XX 03-MAY-1999; 99US-0132287P.
XX XX
XX XX (METH-) METHYLGENE INC.
XX XX
XX XX Macleod AR, Li Z, Besterman JM;
XX PI
XX XX WPI; 2001-016407/02.
XX XX
XX XX Antisense oligonucleotide that inhibits expression of a histone
XX PT deacetylase, useful for treating and/or alleviating the symptoms of
XX PT deacetylase, useful for treating and/or alleviating the symptoms of
XX PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX XX
XX XX Example 1; Page 23; 125pp; English.
XX XX
XX XX The present invention provides inhibitors of histone deacetylase enzymes
XX CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
XX CC inhibitors may be antisense strands or they may be compounds identified
XX CC by contacting the enzyme with the compound and measuring the resulting
XX CC enzyme activity. These inhibitors are useful for treating cancers and for
XX CC identifying which histone deacetylase is involved in a neoplasia
XX XX
XX SQ Sequence 26 BP; 8 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 26; DB 1; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 6.6;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 211 GAATCCGCATGACTCATTAATTGCTG 236
XX DB 26 GAATCCGCATGACTCATTAATTGCTG 1
XX
XX RESULT 5
XX AAC89543/c
XX ID AAC89543 standard; DNA; 26 BP.
XX XX
XX AC AAC89543;
XX XX
XX XX 08-MAR-2001 (first entry)
XX XX
XX XX Human HDAC-1/HDAC-2 antisense sequence SEQ ID NO: 13.
XX DE
XX XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
XX KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
XX KW Gene therapy; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX XX WO200071703-A2.
XX XX
XX XX 30-NOV-2000.
XX XX
XX XX 03-MAY-2000; 2000WO-IB001252.
XX XX
XX XX 03-MAY-1999; 99US-0132287P.
XX XX
XX XX (METH-) METHYLGENE INC.
XX XX
XX XX Macleod AR, Li Z, Besterman JM;
XX PI
XX XX WPI; 2001-016407/02.
XX XX
XX XX Antisense oligonucleotide that inhibits expression of a histone
XX PT deacetylase, useful for treating and/or alleviating the symptoms of
XX PT deacetylase, useful for treating and/or alleviating the symptoms of
XX PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX XX
XX XX Example 1; Page 23; 125pp; English.
XX XX
XX XX The present invention provides inhibitors of histone deacetylase enzymes
XX CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
XX CC inhibitors may be antisense strands or they may be compounds identified
XX CC by contacting the enzyme with the compound and measuring the resulting
```

CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia
 XX
 SQ Sequence 26 BP; 8 A; 5 C; 6 G; 5 T; 2 U; 0 Other;
 Query Match 1.6%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 211 GAATCCGATGACTCATATTTGCTG 236
 DB 26 GAATCCGATGACTCATATTTGCTG 1
 RESULT 6
 ABZ83014/C
 ID ABZ83014 standard; DNA; 27 BP.
 AC ABZ83014;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Toxicologically relevant human PCR primer #173.
 XX
 KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003016500-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 16-AUG-2002; 2002WO-US026514.
 XX
 PR 16-AUG-2001; 2001US-0313080P.
 XX
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX
 PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;
 PI Allen P;
 XX
 WPI; 2003-268322/26.
 XX
 XX
 PT Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.
 XX
 PS Claim 1; Page 99; 455pp; English.
 XX
 CC The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in ABZ82842
 CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
 CC; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals

XX
 SQ Sequence 27 BP; 4 A; 13 C; 2 G; 8 T; 0 U; 0 Other;
 Query Match 1.6%; Score 25.4; DB 1; Length 27;
 Best Local Similarity 96.3%; Pred. No. 8.6;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1528 AAGGGGTCAAGGAGGAGGCAAGTTGG 1554
 DB 27 AAGGGGTCAAGGAGGAGGTCAGTTGG 1
 RESULT 7
 AAC89541/C
 ID AAC89541 standard; DNA; 26 BP.
 XX
 AC AAC89541;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Human HDAC-1/HDAC-2 antisense sequence SEQ ID NO: 11.
 XX
 KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 KW gene therapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2000071703-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 03-MAY-2000; 2000WO-IB001252.
 XX
 PR 03-MAY-1999; 99US-0132287P.
 XX
 PA (METH-) METHYLGENE INC.
 XX
 PI Macleod AR, Li Z, Besterman JM;
 XX
 WPI; 2001-016407/02.
 XX
 PT Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
 XX
 PS Example 1; Page 23; 125pp; English.
 XX
 CC The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia
 XX
 SQ Sequence 26 BP; 7 A; 5 C; 7 G; 5 T; 2 U; 0 Other;
 Query Match 1.5%; Score 24.4; DB 1; Length 26;
 Best Local Similarity 96.2%; Pred. No. 11;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 211 GAATCCGATGACTCATATTTGCTG 236
 DB 26 GAATCCGATGAGCCATATTTGCTG 1
 RESULT 8
 AAC89533/C
 ID AAC89533 standard; DNA; 26 BP.
 XX
 AC AAC89533;
 XX
 DT 08-MAR-2001 (first entry)

Query Match 1.5%; Score 24.4; DB 1; Length 26;
 Best Local Similarity 96.2%; Pred. No. 11;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCGGATGACTCATTAATTGCTG 236
 DB 26 GAATCGGATGACTCATTAATTGCTG 1

RESULT 11
 AAA55837/c
 ID AAA55837 standard; DNA; 26 BP.
 XX
 AC AAA55837;
 XX
 DT 01-SEP-2000 (first entry)
 XX
 DE Histone deacetylase HD1 and HD2 antisense oligonucleotide SEQ ID NO:82.
 XX
 KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200023112-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024278.
 XX
 PR 19-OCT-1998; 98US-0104804P.
 XX
 PY (METH-) METHYLGENE INC.
 XX
 PI Besterman JM, Macleod AR, Siders WM;
 XX
 DR WPI; 2000-339532/29.
 XX
 PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.
 XX
 PS Example 9; Page 58; 99pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention

XX Sequence 26 BP; 7 A; 4 C; 8 G; 5 T; 2 U; 0 Other;

Query Match 1.5%; Score 23.4; DB 1; Length 26;
 Best Local Similarity 96.0%; Pred. No. 15;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGATGACCTCATTAATTGCTG 236
 DB 25 AATCCGATGACCTCATTAATTGCTG 1

RESULT 12
 AAA55838/c
 ID AAA55838 standard; DNA; 26 BP.
 XX
 AC AAA55838;
 XX
 DT 01-SEP-2000 (first entry)
 XX
 DE Histone deacetylase HD1 and HD2 antisense oligonucleotide SEQ ID NO:83.
 XX
 KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200023112-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024278.
 XX
 PR 19-OCT-1998; 98US-0104804P.
 XX
 PY (METH-) METHYLGENE INC.
 XX
 PI Besterman JM, Macleod AR, Siders WM;
 XX
 DR WPI; 2000-339532/29.
 XX
 PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.
 XX
 PS Example 9; Page 58; 99pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention

SQ Sequence 26 BP; 7 A; 4 C; 8 G; 5 T; 2 U; 0 Other;
Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 15;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 212 AATCCGATGACTCATATAATTGCTG 236
Db 25 AATCCGATGACTCATATAATTGCTG 1
RESULT 13
AAAS5802/c
ID AAAS5802 standard; DNA; 23 BP.
XX AC AAAS5802;
XX DT 01-SEP-2000 (first entry)
XX DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:45.
XX KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
XX KW modulation; inhibition; gene expression; combination therapy; p16;
XX KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX KW antiinflammatory; inflammation; asthma; ss.
XX OS Homo sapiens.
XX PN WO200023112-A1.
XX PD 27-APR-2000.
XX PF 19-OCT-1999; 99WO-US024278.
XX PR 19-OCT-1998; 98US-0104804P.
XX PA (METH-) METHYLGENE INC.
XX PI Besterman JM, Macleod AR, Siders WM;
XX DR WPI; 2000-339532/29.
XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX PT with a synergistic amount of antisense oligonucleotide and protein
XX PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX PT of e.g. tumours.
XX PS Disclosure; Page 29; 99pp; English.
XX CC The present invention describes a method for inhibiting the expression of
XX CC a gene in a cell comprising contacting the cell with an effective
XX CC synergistic amount of an antisense oligonucleotide which inhibits
XX CC expression of the gene, and an effective synergistic amount of a protein
XX CC effector of a product of the gene. Also described are: (1) a method for
XX CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX CC comprising an antisense oligonucleotide which inhibits expression of the
XX CC gene in operable association with a protein effector of a gene product;
XX CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX CC methods and compositions are useful as analytical tools for transgenic
XX CC studies and as therapeutic tools, e.g. as gene therapy tools for human
XX CC diseases including benign and malignant tumours, inflammation or asthma.
XX CC The methods, inhibitors and compositions of the invention that inhibit
XX CC expression or activity of a gene or gene product may be used to treat
XX CC patients having, or predisposed to developing, a disease responsive to
XX CC inhibition of the gene. These may also be used to activate silenced genes
XX CC to provide missing gene functions and improve a given condition.
XX CC Furthermore, the methods and compositions are useful as probes of the
XX CC physiological function of a gene product in an experimental cell culture
XX CC or animal system; and to evaluate the effect of inhibiting gene activity
XX CC or expression. AAAS5758 to AAAS5842 represent oligonucleotide sequences
XX CC which are used in the exemplification of the present invention

SQ Sequence 23 BP; 6 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 138 AAAGTCTGTACTACTACGCG 160
Db 23 AAAGTCTGTACTACTACGCG 1
RESULT 14
AAH43112/c
ID AAH43112 standard; DNA; 23 BP.
XX AC AAH43112;
XX DT 19-SEP-2001 (first entry)
XX DE Antisense oligo, target HDAC-1 138-160.
XX KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
XX KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
XX KW fungal infections; ss.
XX OS Synthetic.
XX PN WO200138322-A1.
XX PD 31-MAY-2001.
XX PF 22-NOV-2000; 2000WO-IB001881.
XX PR 23-NOV-1999; 99US-0167035P.
XX PA (METH-) METHYLGENE INC.
XX PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX DR WPI; 2001-432601/46.
XX PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX PT restenosis or fungal infections.
XX PS Disclosure; Page 40; 147pp; English.
XX CC The sequences given in AAH43102-14 are oligonucleotides which are
XX CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
XX CC may be used in combination with an inhibitor of histone deacetylase
XX CC enzyme function, to given an improved inhibitory effect, thereby reducing
XX CC the amount of inhibitor required to obtain a given inhibitory effect.
XX CC Compounds containing these oligonucleotides may be used to treat cell
XX CC proliferation conditions such as cancer, restenosis or psoriasis. They
XX CC can also be used to treat protozoal and fungal infections
XX CC
XX SQ Sequence 23 BP; 6 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 1.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 138 AAAGTCTGTACTACTACGCG 160
Db 23 AAAGTCTGTACTACTACGCG 1
RESULT 15
AAAS5810/c
ID AAAS5810 standard; DNA; 26 BP.
XX AC AAAS5810;

AC	AAH43120;	
XX	19-SEP-2001 (first entry)	
DT		
XX	Antisense oligo, target HDAC-2 211-236.	
DE		
XX	Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;	
KW	cell proliferation; cancer; restenosis; psoriasis; protozoal infection;	
KW	fungal infections; ss.	
XX		
OS	Synthetic.	
XX		
XX	WO200138322-A1.	
XX		
XX	31-MAY-2001.	
XX		
PF	22-NOV-2000; 2000WO-IB001881.	
XX		
XX	23-NOV-1999; 99US-0167035P.	
XX	(METH-) METHYLGENE INC.	
XX		
XX	Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;	
XX		
DR	WPI; 2001-432601/46.	
XX		
PPT	New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-	
PPT	(benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,	
PPT	restenosis or fungal infections.	
XX		
XX	Disclosure; Page 40; 147pp; English.	
XX		
CC	The sequences given in AAH43115-21 are oligonucleotides which are	
CC	antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides	
CC	may be used in combination with an inhibitor of histone deacetylase	
CC	enzyme function, to given an improved inhibitory effect, thereby reducing	
CC	the amount of inhibitor required to obtain a given inhibitory effect.	
CC	Compounds containing these oligonucleotides may be used to treat cell	
CC	proliferation conditions such as cancer, restenosis or psoriasis. They	
CC	can also be used to treat protozoal and fungal infections	
XX		
SQ	Sequence 26 BP; 6 A; 5 C; 8 G; 7 T; 0 U; 0 Other;	
	Query Match 1.4%; Score 22.8; DB 1; Length 26;	
	Best Local Similarity 92.3%; Pred. No. 18;	
	Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	211 GAATCCGCATGACTCATATAATTGCTG 236	
Db	26 GAATCCGCATGACCAACTTGCTG 1	
RESULT 17		
AAAC89535/c		
ID	AAAC89535 standard; DNA; 26 BP.	
XX		
AC	AAAC89535;	
XX		
DT		
XX	08-MAR-2001 (first entry)	
XX		
DE	Human HDAC-1/HDAC-2 PCR primer SEQ ID NO: 5.	
XX		
KW	Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;	
KW	HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;	
KW	gene therapy; PCR primer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200071703-A2.	
XX		
XX	30-NOV-2000.	
XX		
PF	03-MAY-2000; 2000WO-IB001252.	

CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention

XX Sequence 22 BP; 8 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
SQ Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAATTACTATTATGACA 187
Db 22 TTGGAATTACTATTATGACA 1

RESULT 20
AAH43113/c
ID AAH43113 standard; DNA; 22 BP.
XX
AC AAH43113;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 166-187.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Laviole R, Thibault C, Abou-Khalil E;
XX WPI; 2001-432601/46.
XX
DR New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.

CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 22 BP; 8 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGGAATTACTATTATGACA 187
Db 22 TTGGAATTACTATTATGACA 1

RESULT 21
AAA55808/c

AAA55808 standard; DNA; 23 BP.
AAA55808;
01-SEP-2000 (first entry)
Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:53.

Human; DNA methyltransferase; DNA MeTase; antisense oligonucleotide;
modulation; inhibition; gene expression; combination therapy; p16;
histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
methylation; gene therapy; tumour; cytostatic; antiasthmatic;
antiinflammatory; inflammation; asthma; ss.
Homo sapiens.
WO200023112-A1.
27-APR-2000.
19-OCT-1999; 99WO-US024278.
19-OCT-1998; 98US-0104804P.
(METH-) METHYLGENE INC.
Besterman JM, Macleod AR, Siders WM;
WPI; 2000-339532/29.
Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
with a synergistic amount of antisense oligonucleotide and protein
effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
of e.g. tumors.

Disclosure; Page 29; 99pp; English.
The present invention describes a method for inhibiting the expression of
a gene in a cell comprising contacting the cell with an effective
synergistic amount of an antisense oligonucleotide which inhibits
expression of the gene, and an effective synergistic amount of a protein
effector of a product of the gene. Also described are: (1) a method for
treating a disease responsive to inhibition of a gene in a mammal; (2) a
method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
comprising an antisense oligonucleotide which inhibits expression of the
gene in operable association with a protein effector of a gene product;
and (4) a pharmaceutical composition comprising the inhibitor of (3). The
methods and compositions are useful as analytical tools for transgenic
studies and as therapeutic tools, e.g. as gene therapy tools for human
diseases including benign and malignant tumours, inflammation or asthma.
The methods, inhibitors and compositions of the invention that inhibit
expression or activity of a gene or gene product may be used to treat
patients having, or predisposed to developing, a disease responsive to
inhibition of the gene. These may also be used to activate silenced genes
to provide missing gene functions and improve a given condition.
Furthermore, the methods and compositions are useful as probes of the
physiological function of a gene product in an experimental cell culture
or animal system; and to evaluate the effect of inhibiting gene activity
or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
which are used in the exemplification of the present invention

Sequence 23 BP; 5 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAAGTCGTCTACTACTACGACG 160
Db 23 AAAGTCGTCTACTACTACGACG 1

RESULT 22

PN WO200023112-A1.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024278.
XX
XX 19-OCT-1999; 98US-0104804P.
XX
XX (METH-) METHYLGENE INC.
XX
XX Besterman JM, Macleod AR, Siders WM;
XX
XX WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein
XX effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX of e.g. tumors.
XX
XX Disclosure; Page 29; 99pp; English.
XX
XX The present invention describes a method for inhibiting the expression of
XX a gene in a cell comprising contacting the cell with an effective
XX synergistic amount of an antisense oligonucleotide which inhibits
XX expression of the gene, and an effective synergistic amount of a protein
XX effector of a product of the gene. Also described are: (1) a method for
XX treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX comprising an antisense oligonucleotide which inhibits expression of the
XX gene in operable association with a protein effector of a gene product;
XX and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX methods and compositions are useful as analytical tools for transgenic
XX studies and as therapeutic tools, e.g. as gene therapy tools for human
XX diseases including benign and malignant tumours, inflammation or asthma.
XX The methods, inhibitors and compositions of the invention that inhibit
XX expression or activity of a gene or gene product may be used to treat
XX patients having, or predisposed to developing, a disease responsive to
XX inhibition of the gene. These may also be used to activate silenced genes
XX to provide missing gene functions and improve a given condition.
XX Furthermore, the methods and compositions are useful as probes of the
XX physiological function of a gene product in an experimental cell culture
XX or animal system; and to evaluate the effect of inhibiting gene activity
XX or expression. AAA55758 to AAA55942 represent oligonucleotide sequences
XX which are used in the exemplification of the present invention
XX
XX Sequence 22 BP; 9 A; 4 C; 1 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 20.4; DS 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 166 TTGGAATTAATCTATATGACA 187
DB 22 TTGGAATTAATCTATATGACA 1
RESULT 24
AAH43119/c
ID AAH43119 standard; DNA; 22 BP.
XX
XX AAH43119;
AC
XX
XX 19-SEP-2001 (first entry)
DT
XX
XX Antisense oligo, target HDAC-2 166-187.
DE
XX
XX Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
XX Synthetic.
OS
XX
XX WO200138322-A1.
PN 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-IB001881.
XX
XX 23-NOV-1999; 99US-0167035P.
XX
XX (METH-) METHYLGENE INC.
PA
XX
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
XX WPI; 2001-432601/46.
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX PT restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43115-21 are oligonucleotides which are
XX antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
XX may be used in combination with an inhibitor of histone deacetylase
XX enzyme function, to give an improved inhibitory effect, thereby reducing
XX the amount of inhibitor required to obtain a given inhibitory effect.
XX Compounds containing these oligonucleotides may be used to treat cell
XX proliferation conditions such as cancer, restenosis or psoriasis. They
XX can also be used to treat protozoal and fungal infections
XX
XX Sequence 23 BP; 5 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 138 AAAGTCGTGTTACTACTACGACGG 160
DB 23 AAAGTCGTGTTACTACTACGACGG 1
RESULT 23
AAA55809/c
ID AAA55809 standard; DNA; 22 BP.
XX
XX AAA55809;
AC
XX
XX 01-SEP-2000 (first entry)
DT
XX
XX Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:54.
DE
XX
XX Human; DNA methyltransferase; DNA Mase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138322-A1.
PN

AAH43118/c
ID AAH43118 standard; DNA; 23 BP.
XX
XX AAH43118;
AC
XX
XX 19-SEP-2001 (first entry)
DT
XX
XX Antisense oligo, target HDAC-2 138-160.
DE
XX
XX Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
XX Synthetic.
OS
XX
XX WO200138322-A1.
PN 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-IB001881.
XX
XX 23-NOV-1999; 99US-0167035P.
XX
XX (METH-) METHYLGENE INC.
PA
XX
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
XX WPI; 2001-432601/46.
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX PT restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43115-21 are oligonucleotides which are
XX antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
XX may be used in combination with an inhibitor of histone deacetylase
XX enzyme function, to give an improved inhibitory effect, thereby reducing
XX the amount of inhibitor required to obtain a given inhibitory effect.
XX Compounds containing these oligonucleotides may be used to treat cell
XX proliferation conditions such as cancer, restenosis or psoriasis. They
XX can also be used to treat protozoal and fungal infections
XX
XX Sequence 23 BP; 5 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 22;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 138 AAAGTCGTGTTACTACTACGACGG 160
DB 23 AAAGTCGTGTTACTACTACGACGG 1
RESULT 23
AAA55809/c
ID AAA55809 standard; DNA; 22 BP.
XX
XX AAA55809;
AC
XX
XX 01-SEP-2000 (first entry)
DT
XX
XX Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:54.
DE
XX
XX Human; DNA methyltransferase; DNA Mase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200138322-A1.
PN

```

XX 31-MAY-2001.
XX
XX 22-NOV-2000; 200WO-IB001881.
XX
XX 23-NOV-1999; 99US-0167035P.
XX
XX (METH-) METHYLGENE INC.
XX
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX WPI; 2001-432601/46.
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43115-21 are oligonucleotides which are
XX antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
XX may be used in combination with an inhibitor of histone deacetylase
XX enzyme function, to given an improved inhibitory effect, thereby reducing
XX the amount of inhibitor required to obtain a given inhibitory effect.
XX Compounds containing these oligonucleotides may be used to treat cell
XX proliferation conditions such as cancer, restenosis or psoriasis. They
XX can also be used to treat protozoal and fungal infections
XX
XX Sequence 22 BP; 9 A; 4 C; 1 G; 8 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 27;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 166 TTGGAATTAATTACTATTATGGACA 187
Db 22 TTGGAATTAATTATATGGACA 1
XX
RESULT 25
AAAS5793/c
ID AAAS5793 standard; DNA; 20 BP.
XX
XX AAAS5793;
XX
XX 01-SEP-2000 (first entry)
XX
XX Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:36.
XX
XX Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
XX modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
XX
XX WO200023112-A1.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024278.
XX
XX 19-OCT-1998; 98US-0104804P.
XX
XX (METH-) METHYLGENE INC.
XX
XX Besterman JM, Macleod AR, Siders WM;
XX
XX WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein
XX
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
of e.g. tumors.
XX
XX Disclosure; Page 29; 99pp; English.
XX
XX The present invention describes a method for inhibiting the expression of
a gene in a cell comprising contacting the cell with an effective
synergistic amount of an antisense oligonucleotide which inhibits
expression of the gene, and an effective synergistic amount of a protein
effector of a product of the gene. Also described are: (1) a method for
treating a disease responsive to inhibition of a gene in a mammal; (2) a
method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
comprising an antisense oligonucleotide which inhibits expression of the
gene in operable association with a protein effector of a gene product;
and (4) a pharmaceutical composition comprising the inhibitor of (3). The
methods and compositions are useful as analytical tools for transgenic
studies and as therapeutic tools, e.g. as gene therapy tools for human
diseases including benign and malignant tumours, inflammation or asthma.
The methods, inhibitors and compositions of the invention that inhibit
expression or activity of a gene or gene product may be used to treat
patients having, or predisposed to developing, a disease responsive to
inhibition of the gene. These may also be used to activate silenced genes
to provide missing gene functions and improve a given condition.
XX Furthermore, the methods and compositions are useful as probes of the
XX physiological function of a gene product in an experimental cell culture
XX or animal system; and to evaluate the effect of inhibiting gene activity
XX or expression. AAAS5758 to AAAS5842 represent oligonucleotide sequences
XX which are used in the exemplification of the present invention
XX
XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 29 GCTGTCCTCCCACTCGGTGCAT 48
Db 20 GCTGTCCTCCCACTCGGTGCAT 1
XX
RESULT 26
AAAS5792/c
ID AAAS5792 standard; DNA; 20 BP.
XX
XX AAAS5792;
XX
XX 01-SEP-2000 (first entry)
XX
XX Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:35.
XX
XX Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
XX modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
XX
XX WO200023112-A1.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024278.
XX
XX 19-OCT-1998; 98US-0104804P.
XX
XX (METH-) METHYLGENE INC.
XX
XX Besterman JM, Macleod AR, Siders WM;
XX
XX WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein
XX

```

PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.
 XX
 PS Disclosure; Page 29; 99pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC studies and compositions are useful as analytical tools for transgenic
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention
 XX
 SQ Sequence 20 BP; 6 A; 6 C; 8 G; 0 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 CCGCTGGGCGCTGCTC 36
 DB 20 CCGCTGGGCGCTGCTC 1
 RESULT 27
 AAA55794/c
 ID AAA55794 standard; DNA; 20 BP.
 XX
 AC AAA55794;
 XX
 DT 01-SEP-2000 (first entry)
 XX
 DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:37.
 XX
 KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200023112-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024278.
 XX
 PR 19-OCT-1998; 98US-0104804P.
 XX
 XX (METH-) METHYLGENE INC.
 XX
 XX Besterman JM, Macleod AR, Siders WM;
 XX WPI; 2000-339532/29.
 DR

PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.
 XX
 PS Disclosure; Page 29; 99pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention
 XX
 SQ Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 31 TGTCTCCCACTGGTCATCC 50
 DB 20 TGTCTCCCACTGGTCATCC 1
 RESULT 28
 AAA55800/c
 ID AAA55800 standard; DNA; 20 BP.
 XX
 AC AAA55800;
 XX
 DT 01-SEP-2000 (first entry)
 XX
 DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:43.
 XX
 KW Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200023112-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024278.
 XX
 PR 19-OCT-1998; 98US-0104804P.
 XX
 XX (METH-) METHYLGENE INC.
 XX
 XX Besterman JM, Macleod AR, Siders WM;
 XX WPI; 2000-339532/29.
 DR

XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Disclosure; Page 29; 99pp; English.
XX
XX The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
XX Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
SQ

Query Match 1-2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCGGCTTCC 1584
|||
DB 20 CCTCTCCAGCTCGGCTTCC 1

RESULT 29
AAA55795/c
ID AAA55795 standard; DNA; 20 BP.
AC AAA55795;
XX
XX 01-SEP-2000 (first entry)
XX
XX Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:38.
XX
XX Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
OS
XX WO200023112-A1.
PN
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024278.
PF
XX 19-OCT-1998; 98US-0104804P.
PR
XX (METH-) METHYLGENE INC.
XX
XX Besterman JM, Macleod AR, Siders WM;
PI
XX

DR WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
PS Disclosure; Page 29; 99pp; English.
XX
XX The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
XX Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
SQ

Query Match 1-2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCTG 52
|||
DB 20 TCTCCCACTCGGTCATCTG 1

RESULT 30
AAA55796/c
ID AAA55796 standard; DNA; 20 BP.
AC AAA55796;
XX
XX 01-SEP-2000 (first entry)
XX
XX Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:39.
XX
XX Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
OS
XX WO200023112-A1.
PN
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024278.
PF
XX 19-OCT-1998; 98US-0104804P.
PR
XX (METH-) METHYLGENE INC.
XX
XX Besterman JM, Macleod AR, Siders WM;
PI
XX

XX WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.
XX
XX Disclosure; Page 29; 99pp; English.
XX
XX The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTCATCCTGAGAACACA 60
|||
DB 20 TCGGTCATCCTGAGAACACA 1

RESULT 31
AAA55801/c
ID AAA55801 standard; DNA; 20 BP.

XX AC AAA55801;

XX DT 01-SEP-2000 (first entry)

XX DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:44.

XX Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.

XX OS Homo sapiens.

XX PN WO2000023112-A1.

XX PD 27-APR-2000.

XX PF 19-OCT-1999; 99WO-US024278.

XX PR 19-OCT-1998; 98US-0104804P.

XX PA (METH-) METHYLGENE INC.

PI Besterman JM, Macleod AR, Siders WM;
XX WPI; 2000-339532/29.

XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
PT with a synergistic amount of antisense oligonucleotide and protein
PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
PT of e.g. tumors.

XX Disclosure; Page 29; 99pp; English.

XX The present invention describes a method for inhibiting the expression of
CC a gene in a cell comprising contacting the cell with an effective
CC synergistic amount of an antisense oligonucleotide which inhibits
CC expression of the gene, and an effective synergistic amount of a protein
CC effector of a product of the gene. Also described are: (1) a method for
CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
CC comprising an antisense oligonucleotide which inhibits expression of the
CC gene in operable association with a protein effector of a gene product;
CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
CC methods and compositions are useful as analytical tools for transgenic
CC studies and as therapeutic tools, e.g. as gene therapy tools for human
CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX

XX Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGGTTTC 1604
|||
DB 20 TGCTGAGTCCCTCAGGTTTC 1

RESULT 32
AAA55798/c

ID AAA55798 standard; DNA; 20 BP.

XX AC AAA55798;

XX DT 01-SEP-2000 (first entry)

XX DE Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:41.

XX Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
KW modulation; inhibition; gene expression; combination therapy; p16;
KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
KW antiinflammatory; inflammation; asthma; ss.

XX OS Homo sapiens.

XX PN WO2000023112-A1.

XX PD 27-APR-2000.

XX PF 19-OCT-1999; 99WO-US024278.

XX PR 19-OCT-1998; 98US-0104804P.

XX PA (METH-) METHYLGENE INC.

```

XX PI Besterman JM, Macleod AR, Siders WM;
XX DR WPI; 2000-339532/29.
XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX PT with a synergistic amount of antisense oligonucleotide and protein
XX PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX PT of e.g. tumors.
XX PS Disclosure; Page 29; 99pp; English.
XX CC The present invention describes a method for inhibiting the expression of
XX CC a gene in a cell comprising contacting the cell with an effective
XX CC synergistic amount of an antisense oligonucleotide which inhibits
XX CC expression of the gene, and an effective synergistic amount of a protein
XX CC effector of a product of the gene. Also described are: (1) a method for
XX CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX CC comprising an antisense oligonucleotide which inhibits expression of the
XX CC gene in operable association with a protein effector of a gene product;
XX CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX CC methods and compositions are useful as analytical tools for transgenic
XX CC studies and as therapeutic tools, e.g. as gene therapy tools for human
XX CC diseases including benign and malignant tumours, inflammation or asthma.
XX CC The methods, inhibitors and compositions of the invention that inhibit
XX CC expression or activity of a gene or gene product may be used to treat
XX CC patients having, or predisposed to developing, a disease responsive to
XX CC inhibition of the gene. These may also be used to activate silenced genes
XX CC to provide missing gene functions and improve a given condition.
XX CC Furthermore, the methods and compositions are useful as probes of the
XX CC physiological function of a gene product in an experimental cell culture
XX CC or animal system; and to evaluate the effect of inhibiting gene activity
XX CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
XX CC which are used in the exemplification of the present invention
XX SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 33
AAH43108/c
ID AAH43108 standard; DNA; 20 BP.
AC AAH43108;
XX 19-SEP-2001 (first entry)
XX DE Antisense oligo, target HDAC-1 1504-1523.
XX KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
XX KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
XX KW fungal infections; ss.
XX OS Synthetic.
XX PN WO200138322-A1.
XX PD 31-MAY-2001.
XX PF 22-NOV-2000; 2000WO-1B001881.
XX PR 23-NOV-1999; 99US-0167035P.
XX PA (METH-) METHYLGENE INC.
XX PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX DR WPI; 2001-432601/46.
XX PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX PT restenosis or fungal infections.
XX PS Disclosure; Page 40; 147pp; English.
XX CC The sequences given in AAH43102-14 are oligonucleotides which are
XX CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
XX CC may be used in combination with an inhibitor of histone deacetylase
XX CC enzyme function, to given an improved inhibitory effect, thereby reducing
XX CC the amount of inhibitor required to obtain a given inhibitory effect.
XX CC Compounds containing these oligonucleotides may be used to treat cell
XX CC proliferation conditions such as cancer, restenosis or psoriasis. They
XX CC can also be used to treat protozoal and fungal infections
XX SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 34
AAH43105/c
ID AAH43105 standard; DNA; 20 BP.
AC AAH43105;
XX 19-SEP-2001 (first entry)
XX DE Antisense oligo, target HDAC-1 33-52.
XX KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
XX KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
XX KW fungal infections; ss.
XX OS Synthetic.
XX PN WO200138322-A1.
XX PD 31-MAY-2001.
XX PF 22-NOV-2000; 2000WO-1B001881.
XX PR 23-NOV-1999; 99US-0167035P.
XX PA (METH-) METHYLGENE INC.
XX PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX DR WPI; 2001-432601/46.
XX PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX PT restenosis or fungal infections.
XX PS Disclosure; Page 40; 147pp; English.
XX CC The sequences given in AAH43102-14 are oligonucleotides which are
XX CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
XX CC may be used in combination with an inhibitor of histone deacetylase
XX CC enzyme function, to given an improved inhibitory effect, thereby reducing
XX CC the amount of inhibitor required to obtain a given inhibitory effect.
XX CC Compounds containing these oligonucleotides may be used to treat cell
XX CC proliferation conditions such as cancer, restenosis or psoriasis. They
XX CC can also be used to treat protozoal and fungal infections

```

CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCACTCG 52
DB 20 TCTCCCACTCGGTCACTCG 1

RESULT 35
AAH43102/c
ID AAH43102 standard; DNA; 20 BP.

XX
AC AAH43102;

XX 19-SEP-2001 (first entry)

XX Antisense oligo, target HDAC-1 17-36.

XX Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.

XX Synthetic.

XX WO200138322-A1.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-IB001881.

XX 23-NOV-1999; 99US-0167035P.

XX (METH-) METHYLGENE INC.

PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;

XX WPI; 2001-432601/46.

XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.

PS Disclosure; Page 40; 147pp; English.

CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections

XX Sequence 20 BP; 6 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCCGCTGGTGGTGGTGGTTC 36
DB 20 CCCGCTGGTGGTGGTGGTTC 1

RESULT 36
AAH43111/c
ID AAH43111 standard; DNA; 20 BP.

XX

AC AAH43111;

XX 19-SEP-2001 (first entry)

XX Antisense oligo, target HDAC-1 1585-1604.

XX Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.

XX Synthetic.

XX WO200138322-A1.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-IB001881.

XX 23-NOV-1999; 99US-0167035P.

XX (METH-) METHYLGENE INC.

XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;

XX WPI; 2001-432601/46.

XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.

PS Disclosure; Page 40; 147pp; English.

CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections

XX Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604

DB 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 37

AAH43106/c

ID AAH43106 standard; DNA; 20 BP.

XX

XX 19-SEP-2001 (first entry)

XX Antisense oligo, target HDAC-1 41-60.

XX Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.

XX Synthetic.

XX WO200138322-A1.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-IB001881.

PF

XX 23-NOV-1999; 99US-0167035P.
XX (METH-) METHYLGENE INC.
XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX WPI; 2001-432601/46.
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43102-14 are oligonucleotides which are
XX antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
XX may be used in combination with an inhibitor of histone deacetylase
XX enzyme function, to give an improved inhibitory effect, thereby reducing
XX the amount of inhibitor required to obtain a given inhibitory effect.
XX Compounds containing these oligonucleotides may be used to treat cell
XX proliferation conditions such as cancer, restenosis or psoriasis. They
XX can also be used to treat protozoal and fungal infections
XX
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 TCGGTCATCCTGAGAACACA 60
DB 20 TCGGTCATCCTGAGAACACA 1
RESULT 38
AAH43104/C
ID AAH43104 standard; DNA; 20 BP.
AC AAH43104;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 31-50.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
XX (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
XX restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43102-14 are oligonucleotides which are
XX antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides

CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
XX Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 TGTCTCCCACTCGGTATCC 50
DB 20 TGTCTCCCACTCGGTATCC 1
RESULT 39
AAH43110/C
ID AAH43110 standard; DNA; 20 BP.
XX
AC AAH43110;
XX
DT 19-SEP-2001 (first entry)
XX
DE Antisense oligo, target HDAC-1 1565-1584.
XX
KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
KW fungal infections; ss.
XX
OS Synthetic.
XX
PN WO200138322-A1.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-IB001881.
XX
PR 23-NOV-1999; 99US-0167035P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
XX
DR WPI; 2001-432601/46.
XX
PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
XX Disclosure; Page 40; 147pp; English.
XX
XX The sequences given in AAH43102-14 are oligonucleotides which are
XX antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
XX may be used in combination with an inhibitor of histone deacetylase
XX enzyme function, to give an improved inhibitory effect, thereby reducing
XX the amount of inhibitor required to obtain a given inhibitory effect.
XX Compounds containing these oligonucleotides may be used to treat cell
XX proliferation conditions such as cancer, restenosis or psoriasis. They
XX can also be used to treat protozoal and fungal infections
XX
XX Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
DB 20 CCTCTCCAGCTCTGGCTTCC 1

PN WO200071703-A2.
 XX 30-NOV-2000.
 XX 03-MAY-2000; 2000WO-IB001252.
 XX 03-MAY-1999; 99US-0132287P.
 XX (METH-) METHYLGENE INC.
 XX Macleod AR, Li Z, Besterman JM;
 XX WPI; 2001-016407/02.
 XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
 XX Example 1; Page 23; 125pp; English.
 XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia
 XX SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1585 TGCTGAGTCCCTCAGTTTC 1604
 DB 20 TGCTGAGTCCCTCAGTTTC 1
 RESULT 42
 AAC89531/c
 ID AAC89531 standard; DNA; 20 BP.
 XX AAC89531;
 XX 08-MAR-2001 (first entry)
 DT Human HDAC-1 PCR primer SEQ ID NO: 1.
 XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 XX HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 XX Gene therapy; PCR primer; ss.
 XX Homo sapiens.
 XX WO200071703-A2.
 XX 30-NOV-2000.
 XX 03-MAY-2000; 2000WO-IB001252.
 XX 03-MAY-1999; 99US-0132287P.
 XX (METH-) METHYLGENE INC.
 XX Macleod AR, Li Z, Besterman JM;
 XX WPI; 2001-016407/02.
 XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
 XX Example 2; Page 12; 125pp; English.

PN WO2000138322-A1.
 XX 31-MAY-2001.
 XX 22-NOV-2000; 2000WO-IB001981.
 XX 23-NOV-1999; 99US-0167035P.
 XX (METH-) METHYLGENE INC.
 XX Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;
 XX WPI; 2001-432601/46.
 XX New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
 PT (benzenesulfonfylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
 PT restenosis or fungal infections.
 XX Disclosure; Page 40; 147pp; English.
 XX The sequences given in AAH43102-14 are oligonucleotides which are
 CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
 CC may be used in combination with an inhibitor of histone deacetylase
 CC enzyme function, to give an improved inhibitory effect, thereby reducing
 CC the amount of inhibitor required to obtain a given inhibitory effect.
 CC Compounds containing these oligonucleotides may be used to treat cell
 CC proliferation conditions such as cancer, restenosis or psoriasis. They
 CC can also be used to treat protozoal and fungal infections
 XX SQ Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 GCTGTCTCCCACTCGGTCAAT 48
 DB 20 GCTGTCTCCCACTCGGTCAAT 1
 RESULT 41
 AAC89540/c
 ID AAC89540 standard; DNA; 20 BP.
 XX AAC89540;
 XX 08-MAR-2001 (first entry)
 DT Human HDAC-1 antisense sequence SEQ ID NO: 10.
 XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 XX HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 XX Gene therapy; PCR primer; ss.
 XX Homo sapiens.
 XX

XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1585 TGCTGAGTCCCTCACGTTTC 1604
 DB 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 43
 AAD20115/C
 ID AAD20115 standard; DNA; 20 BP.
 XX
 AC AAD20115;
 DT 03-JAN-2002 (first entry)
 XX Human histone deacetylase antisense oligonucleotide, HDAC1 AS1.
 DE
 XX Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor;
 KW HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis;
 KW protozoal disease; fungal disease; infection; ss.
 XX Homo sapiens.
 OS
 XX WO200170675-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 26-MAR-2001; 2001WO-1B000683.
 XX
 PR 24-MAR-2000; 2000US-0192151P.
 XX
 PA (METH-) METHYLGENE INC.
 XX
 PI Delorme D, Woc SH, Vaisburg A;
 XX
 DR WPI; 2001-639108/73.

XX An inhibitor of histone deacetylase for the treatment of cell
 PT proliferation diseases and conditions such as cancer, restenosis or
 PT psoriasis or preventing protozoal or fungal disease or infections.
 XX
 PS Disclosure; Page 54; 241pp; English.

XX The present invention relates to compounds and methods for inhibiting
 CC histone deacetylase (HDAC) enzymatic activity. Compounds of the invention
 CC are used for the treatment of cell proliferative diseases and conditions
 CC such as cancer, restenosis or psoriasis. They are also used for treating
 CC or preventing protozoal or fungal disease or infections. The present
 CC sequence is antisense oligonucleotide, HDAC1 AS1 which is targeted to
 CC the 3' untranslated region (UTR) of human HDAC1 to inhibit its enzymatic
 CC activity
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1585 TGCTGAGTCCCTCACGTTTC 1604
 DB 20 TGCTGAGTCCCTCACGTTTC 1

RESULT 44
 AAD20116/C
 ID AAD20116 standard; DNA; 20 BP.
 XX
 AC AAD20116;
 DT 03-JAN-2002 (first entry)
 XX
 DE Human histone deacetylase antisense oligonucleotide, HDAC1 AS2.
 XX
 XX Human; cytostatic; vasotropic; fungicide; histone deacetylase; inhibitor;
 KW HDAC; therapy; cell proliferative disease; cancer; restenosis; psoriasis;
 KW protozoal disease; fungal disease; infection; ss.
 XX Homo sapiens.
 OS
 XX WO200170675-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 26-MAR-2001; 2001WO-1B000683.
 XX
 PR 24-MAR-2000; 2000US-0192151P.
 XX
 PA (METH-) METHYLGENE INC.
 XX
 PI Delorme D, Woc SH, Vaisburg A;
 XX
 DR WPI; 2001-639108/73.

XX An inhibitor of histone deacetylase for the treatment of cell
 PT proliferation diseases and conditions such as cancer, restenosis or
 PT psoriasis or preventing protozoal or fungal disease or infections.
 XX
 PS Disclosure; Page 54; 241pp; English.

XX The present invention relates to compounds and methods for inhibiting
 CC histone deacetylase (HDAC) enzymatic activity. Compounds of the invention
 CC are used for the treatment of cell proliferative diseases and conditions
 CC such as cancer, restenosis or psoriasis. They are also used for treating
 CC or preventing protozoal or fungal disease or infections. The present
 CC sequence is antisense oligonucleotide, HDAC1 AS2 which is targeted to
 CC the 3' untranslated region (UTR) of human HDAC1 to inhibit its enzymatic
 CC activity
 XX
 SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
 DB 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 45
 AAD40908/C
 ID AAD40908 standard; DNA; 20 BP.
 XX
 AC AAD40908;
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAC1 antisense oligonucleotide ISIS #123689.
 XX
 KW Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX
 OS Homo sapiens.

OS XX XX Synthetic.

PH XX Key Location/Qualifiers

FT FT modified_base 1..20

FT FT /*tag= a

FT FT /mod_base= OTHER

FT FT /note= "Phosphorothioate backbone"

FT FT modified_base 1..5

FT FT /*tag= b

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl residues"

FT FT modified_base 1..4

FT FT /*tag= d

FT FT /mod_base= m5c

FT FT modified_base 9..10

FT FT /*tag= e

FT FT /mod_base= m5c

FT FT modified_base 16..20

FT FT /*tag= c

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl residues"

FT FT modified_base 20

FT FT /*tag= f

FT FT /mod_base= m5c

XX XX WO200250244-A2.

PN XX 27-JUN-2002.

XX XX 07-DEC-2001; 2001WO-US046518.

XX XX 19-DEC-2000; 2000US-00745167.

XX XX (ISIS-) ISIS PHARM INC.

XX XX Monia BP, Wyatt JR;

XX XX WPI; 2002-519880/55.

XX XX Antisense compounds targeted against polynucleotides encoding Histone

XX XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.

XX XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral

XX XX infection.

XX XX Claim 3; Page 93; 120pp; English.

XX XX The present invention relates to antisense compounds, compositions and

XX XX methods for modulating the expression of Histone deacetylase 1 (HDAL).

XX XX Sequences of the invention are useful for inhibiting the expression of

XX XX HDAL in cells or tissues and for treating an animal having a disease or

XX XX condition associated with HDAL e.g., hyperproliferative condition, which

XX XX is cancer of haematopoietic, lymphoid, myeloid or breast or a condition

XX XX resulting from a viral infection. Antisense compounds either alone or in

XX XX combination with other antisense compounds or therapeutics can be used as

XX XX tools in differential and/or combinatorial analyses to elucidate the

XX XX expression patterns of a portion or the entire complement of genes

XX XX reagents and diagnostics. They may also be useful prophylactically such

XX XX as to prevent or delay infection, inflammation or tumour formation. The

XX XX present DNA sequence is an antisense oligonucleotide targeted to human

XX XX HDAL DNA

SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No.26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 GTACTTCCAGAACTGGG 738

DB 20 GTACTTCCAGAACTGGG 1

RESULT 46

AAD40910/c

ID AAD40910 standard; DNA; 20 BP.

XX AC AAD40910;

XX DT 30-OCT-2002 (first entry)

XX DE Human HDAL antisense oligonucleotide ISIS #123691.

XX KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;

XX KW viral infection; prophylactic; inflammation; phosphorothioate backbone;

XX KW tumour; antisense; cytostatic; virucide; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PH Key Location/Qualifiers

FT FT modified_base 1..20

FT FT /*tag= a

FT FT /mod_base= OTHER

FT FT /note= "Phosphorothioate backbone"

FT FT modified_base 1..5

FT FT /*tag= b

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl residues"

FT FT modified_base 2..4

FT FT /*tag= d

FT FT /mod_base= m5c

FT FT modified_base 11..14

FT FT /*tag= e

FT FT /mod_base= m5c

FT FT modified_base 16..20

FT FT /*tag= c

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl residues"

FT FT modified_base 19..20

FT FT /*tag= f

FT FT /mod_base= m5c

XX XX WO200250244-A2.

PN XX 27-JUN-2002.

XX XX 07-DEC-2001; 2001WO-US046518.

XX XX 19-DEC-2000; 2000US-00745167.

XX XX (ISIS-) ISIS PHARM INC.

XX XX Monia BP, Wyatt JR;

XX XX WPI; 2002-519880/55.

XX XX Antisense compounds targeted against polynucleotides encoding Histone

XX XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.

XX XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral

XX XX infection.

XX XX Claim 3; Page 93; 120pp; English.

XX XX The present invention relates to antisense compounds, compositions and

XX XX methods for modulating the expression of Histone deacetylase 1 (HDAL).

XX XX Sequences of the invention are useful for inhibiting the expression of

XX XX HDAL in cells or tissues and for treating an animal having a disease or

XX XX condition associated with HDAL e.g., hyperproliferative condition, which

XX XX is cancer of haematopoietic, lymphoid, myeloid or breast or a condition

XX XX resulting from a viral infection. Antisense compounds either alone or in

XX XX combination with other antisense compounds or therapeutics can be used as

XX XX tools in differential and/or combinatorial analyses to elucidate the

XX XX expression patterns of a portion or the entire complement of genes

XX XX reagents and diagnostics. They are commonly used as research

XX XX as to prevent or delay infection, inflammation or tumour formation. The

XX XX present DNA sequence is an antisense oligonucleotide targeted to human

XX XX HDAL DNA

CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 729 GGAAGTGGGACCTACGGGA 748
Db 20 GGAAGTGGGACCTACGGGA 1
RESULT 47
ID AAD40912/c
AC AAD40912;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAL antisense oligonucleotide ISIS #123693.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1
FT /tag= d
FT /mod_base= m5c
FT modified_base 5..7
FT /tag= e
FT /mod_base= m5c
FT modified_base 10
FT /tag= f
FT /mod_base= m5c
FT modified_base 12
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= h
FT /mod_base= m5c
WC2002050244-A2.
XX
PN 27-JUN-2002.
XX
PD 07-DEC-2001; 2001WO-US04518.
XX
PF 19-DEC-2000; 2000US-00745167.
XX
PR (ISIS-) ISIS PHARM INC.
XX
PA Monia BP, Wyatt JR;
PI
XX

DR WPI; 2002-519880/55.
XX
FT Antisense compounds targeted against polynucleotides encoding Histone
FT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
FT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
FT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 788 CCGCTCCGAGACGGGATTG 807
Db 20 CCGCTCCGAGACGGGATTG 1
RESULT 48
AAD40913/c
ID AAD40913 standard; DNA; 20 BP.
XX
AC AAD40913;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAL antisense oligonucleotide ISIS #123694.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 6..7
FT /tag= d
FT /mod_base= m5c
FT modified_base 9
FT /tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 16
FT

FT FT /*tag= f
FT /mod_base= m5c
FT modified_base 18
FT /*tag= g
FT /mod_base= m5c
XX PN WO200250244-A2.
XX 27-JUN-2002.
XX PD
XX PF 07-DEC-2001; 2001WO-US046518.
XX PR 19-DEC-2000; 2000US-00745167.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX DR
XX FT Antisense compounds targeted against polynucleotides encoding Histone
FT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX PS Claim 3; Page 94; 120pp; English.
XX CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAl DNA
XX SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Indels 0; Gaps 0;
QY 811 ACGAGTCCTATGAGGCCATT 830
DB 20 ACGAGTCCTATGAGGCCATT 1
RESULT 49
AAD40926/c
ID AAD40926 standard; DNA; 20 BP.
XX AC AAD40926;
XX AC
XX 30-OCT-2002 (first entry)
XX DE Human HDAl antisense oligonucleotide ISIS #123707.
XX KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT modified_base 1.20

FT FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT 1.5
FT modified_base
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT 6
FT modified_base
FT /*tag= d
FT /mod_base= m5c
FT 9
FT modified_base
FT /*tag= e
FT /mod_base= m5c
FT 11.12
FT modified_base
FT /*tag= f
FT /mod_base= m5c
FT 16.20
FT modified_base
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT 18
FT modified_base
FT /*tag= g
FT /mod_base= m5c
FT 20
FT modified_base
FT /*tag= h
FT /mod_base= m5c
XX PN WO200250244-A2.
XX PD 27-JUN-2002.
XX PF 07-DEC-2001; 2001WO-US046518.
XX PR 19-DEC-2000; 2000US-00745167.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX DR
XX FT Antisense compounds targeted against polynucleotides encoding Histone
FT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX PS Claim 3; Page 94; 120pp; English.
XX CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAl DNA
XX SQ Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Indels 0; Gaps 0;
QY 1179 GAGTACCTGGAGAGATCAA 1198
DB 20 GAGTACCTGGAGAGATCAA 1

CC methods for modulating the expression of Histone deacetylase 1 (HDAC1).
 CC Sequences of the invention are useful for inhibiting the expression of
 CC HDAC1 in cells or tissues and for treating an animal having a disease or
 CC condition associated with HDAC1 e.g., hyperproliferative condition, which
 CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
 CC resulting from a viral infection. Antisense compounds either alone or in
 CC combination with other antisense compounds or therapeutics can be used as
 CC tools in differential and/or combinatorial analyses to elucidate the
 CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targetted to human
 CC HDAC1 DNA
 XX
 SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1509 GAGGAGAGCCGAGAGCCAA 1528
 DB 20 GAGGAGAGCCGAGAGCCAA 1
 RESULT 51
 AAD40893/c
 ID AAD40893 standard; DNA; 20 BP.
 XX
 AC AAD40893;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAC1 antisense oligonucleotide ISIS #123674.
 XX
 KW Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= m5c
 FT modified_base 1..20
 FT /tag= c
 FT /mod_base= m5c
 FT modified_base 1..20
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 1..20
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 1..20
 FT /tag= f
 FT /mod_base= m5c
 FT modified_base 1..20
 FT /tag= g
 FT /mod_base= m5c
 FT modified_base 1..20
 FT /tag= h
 FT /mod_base= m5c
 FT modified_base 1..20
 FT /tag= i
 FT /mod_base= m5c
 XX WO200250244-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 07-DEC-2001; 2001WO-US046518.
 XX
 XX 19-DEC-2000; 2000US-00745167.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Wyatt JR;
 XX WPI; 2002-519880/55.
 DR
 XX Antisense compounds targeted against polynucleotides encoding Histone
 XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 XX infection.
 XX
 PS Claim 3; Page 94; 120pp; English.
 XX
 CC The present invention relates to antisense compounds, compositions and

RESULT 50
 AAD40935/c
 ID AAD40935 standard; DNA; 20 BP.
 XX
 AC AAD40935;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAC1 antisense oligonucleotide ISIS #123716.
 XX
 KW Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 5
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 8
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 12
 FT /tag= f
 FT /mod_base= m5c
 FT modified_base 15
 FT /tag= g
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 17..18
 FT /tag= h
 FT /mod_base= m5c
 FT modified_base 20
 FT /tag= i
 FT /mod_base= m5c
 XX WO200250244-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 07-DEC-2001; 2001WO-US046518.
 XX
 XX 19-DEC-2000; 2000US-00745167.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Wyatt JR;
 XX WPI; 2002-519880/55.
 DR
 XX Antisense compounds targeted against polynucleotides encoding Histone
 XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 XX infection.
 XX
 PS Claim 3; Page 94; 120pp; English.
 XX
 CC The present invention relates to antisense compounds, compositions and

```

PF 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAl DNA
XX
XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 278 TCACAAAGCCCAATGCTGAGG 297
Db 20 TCACAAAGCCCAATGCTGAGG 1
XX
XX RESULT 52
XX AAD40887/c
XX ID AAD40887 standard; DNA; 20 BP.
XX
XX AC AAD40887;
XX
XX DT 30-OCT-2002 (first entry)
XX
XX DE Human HDAl antisense oligonucleotide ISIS #123668.
XX
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "phosphorothioate backbone"
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl residues"
XX modified_base 9
XX /tag= d
XX /mod_base= m5c
XX

```

```

FT modified_base 13
FT /tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17..18
FT /tag= f
FT /mod_base= m5c
FT modified_base 20
FT /tag= g
FT /mod_base= m5c
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAl DNA
XX
XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 134 GAGGAAAGTCGTTACTACT 153
Db 20 GAGGAAAGTCGTTACTACT 1
XX
XX RESULT 53
XX AAD40892/c
XX ID AAD40892 standard; DNA; 20 BP.
XX
XX AC AAD40892;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123673.
XX
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX

```

KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 XX tumour; antisense; cytosstatic; virucide; ss.
 OS Homo sapiens.
 XX Synthetic.

PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 2
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 8
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 19
 FT /tag= f
 FT /mod_base= m5c

XX WO200250244-A2.
 PN
 XX
 XX 27-JUN-2002.
 XX
 XX 07-DEC-2001; 2001WO-US046518.
 XX
 XX 19-DEC-2000; 2000US-00745167.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Monia BP, Wyatt JR;
 PI
 XX WPI; 2002-519880/55.
 DR
 XX Antisense compounds targeted against polynucleotides encoding Histone
 PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 PT infection.
 PT
 XX Claim 3; Page 93; 120pp; English.

CC The present invention relates to antisense compounds, compositions and
 CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
 CC Sequences of the invention are useful for inhibiting the expression of
 CC HDAl in cells or tissues and for treating an animal having a disease or
 CC condition associated with HDAl e.g., hyperproliferative condition, which
 CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
 CC resulting from a viral infection. Antisense compounds either alone or in
 CC combination with other antisense compounds or therapeutics can be used as
 CC tools in differential and/or combinatorial analyses to elucidate the
 CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targetted to human
 CC HDAl DNA
 CC
 XX
 XX Sequence 20 BP; 2 A; 3 C; 9 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1..2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 CGCCTCACAAAGCCAATGC 292

Db 20 CGCCTCACAAAGCCAATGC 1
 RESULT 54
 RAD40897/c
 ID AAD40897 standard; DNA; 20 BP.
 XX
 AC AAD40897;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAl antisense oligonucleotide ISIS #123678.
 XX
 KW Human, histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
 RW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytosstatic; virucide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.

PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 1
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 3
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 6
 FT /tag= f
 FT /mod_base= m5c
 FT modified_base 9
 FT /tag= g
 FT /mod_base= m5c
 FT modified_base 12
 FT /tag= h
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 16
 FT /tag= i
 FT /mod_base= m5c

XX WO200250244-A2.
 XX
 XX 27-JUN-2002.
 XX
 XX 07-DEC-2001; 2001WO-US046518.
 XX
 XX 19-DEC-2000; 2000US-00745167.
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Wyatt JR;
 XX
 XX WPI; 2002-519880/55.
 XX
 XX Antisense compounds targeted against polynucleotides encoding Histone
 PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 PT infection.
 XX
 XX Claim 3; Page 93; 120pp; English.

XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DE 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 TACAGCAGCAGATGCAGAG 388
Db 20 TACAGCAGCAGATGCAGAG 1

RESULT 55
AAD40925/c
ID AAD40925 standard; DNA; 20 BP.

XX AAD40925;

XX 30-OCT-2002 (first entry)

DE Human HDAL antisense oligonucleotide ISIS #123706.

XX Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT modified_base 2
FT /note= "2'-methoxyethyl residues"
FT /tag= d
FT /mod_base= m5c
FT modified_base 4..5
FT /tag= e
FT /mod_base= m5c
FT modified_base 11
FT /tag= f
FT /mod_base= m5c
FT modified_base 13
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= h
FT /mod_base= m5c

XX WO200250244-A2.

XX 27-JUN-2002.

XX 07-DEC-2001; 2001WO-US046518.

XX 19-DEC-2000; 2000US-00745167.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.

XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.

XX Claim 3; Page 94; 120pp; English.

XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAL DNA

XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1172 CACGAATGAGTACCTGGAGA 1191

Db 20 CACGAATGAGTACCTGGAGA 1

RESULT 56

AAD40932/c

ID AAD40932 standard; DNA; 20 BP.

XX AAD40932;

XX 30-OCT-2002 (first entry)

XX Human HDAL antisense oligonucleotide ISIS #123713.

XX Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.

XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b

```

FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base
FT 5 /tag= d
FT /mod_base= m5c
FT modified_base
FT 9 /tag= e
FT /mod_base= m5c
FT modified_base
FT 11 /tag= f
FT /mod_base= m5c
FT modified_base
FT 16..20 /tag= c
FT /mod_base= OTHER
FT modified_base
FT 17 /tag= g
FT /mod_base= m5c
FT modified_base
FT 20 /tag= h
FT /mod_base= m5c
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 94; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAl DNA
XX
XX Sequence 20 BP; 1 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1449 GATGAAAAAGAGAAAGACC 1468
XX |||||
XX Db 20 GATGAAAAAGAGAAAGACC 1
XX
XX RESULT 57
XX AAD40937/c
XX ID AAD40937 standard; DNA; 20 BP.

```

```

XX AAD40937;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123718.
XX
XX Human, histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Location/Qualifiers
XX Key modified_base
XX 1..20 /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base
XX 1..5 /tag= b
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl residues"
XX modified_base
XX 5..6 /tag= d
XX /mod_base= m5c
XX modified_base
XX 10 /tag= e
XX /mod_base= m5c
XX modified_base
XX 14..15 /tag= f
XX /mod_base= m5c
XX modified_base
XX 16..20 /tag= c
XX /mod_base= OTHER
XX modified_base
XX 18 /tag= g
XX /mod_base= m5c
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 94; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAl DNA
XX
XX Sequence 20 BP; 1 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1449 GATGAAAAAGAGAAAGACC 1468
XX |||||
XX Db 20 GATGAAAAAGAGAAAGACC 1
XX
XX RESULT 57
XX AAD40937/c
XX ID AAD40937 standard; DNA; 20 BP.

```

CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targetted to human
 CC HDAl DNA

XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1548 AAGTTGGCCTGAATGGACCT 1567
 Db 20 AAGTTGGCCTGAATGGACCT 1

RESULT 58
 ID AAD40938 standard; DNA; 20 BP.
 XX AAD40938;
 AC AAD40938;
 DT 30-OCT-2002 (first entry)
 XX Human HDAl antisense oligonucleotide ISIS #123719.
 DE Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 6..7
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 12
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 XX WO200250244-A2.
 EN 27-JUN-2002.
 PD 07-DEC-2001; 2001WO-US046518.
 PF 19-DEC-2000; 2000US-00745167.
 PR (ISIS-) ISIS PHARM INC.
 XX Monia BP, Wyatt JR;
 PI WPI; 2002-519880/55.
 DR Antisense compounds targetted against polynucleotides encoding Histone
 FT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 PT infection.
 XX Claim 3; Page 94; 120pp; English.

CC The present invention relates to antisense compounds, compositions and
 CC methods for modulating the expression of histone deacetylase 1 (HDAl).
 CC Sequences of the invention are useful for inhibiting the expression of
 CC HDAl in cells or tissues and for treating an animal having a disease or
 CC condition associated with HDAl e.g., hyperproliferative condition, which
 CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
 CC resulting from a viral infection. Antisense compounds either alone or in
 CC combination with other antisense compounds or therapeutics can be used as
 CC tools in differential and/or combinatorial analyses to elucidate the
 CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targetted to human
 CC HDAl DNA

XX Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 CCTCTCCAGCTCTGGCTTCC 1584
 Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 59
 ID AAD40886 standard; DNA; 20 BP.
 XX AAD40886;
 AC AAD40886;
 DT 30-OCT-2002 (first entry)
 XX Human HDAl antisense oligonucleotide ISIS #123667.
 DE Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 2
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 5
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 7..8
 FT /tag= f
 FT /mod_base= m5c
 FT modified_base 11
 FT /tag= g
 FT /mod_base= m5c
 FT modified_base 15
 FT /tag= h
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 17

FT FT /*tag= i
FT /mod_base= m5c
FT modified_base 19..20
FT /*tag= j
FT /mod_base= m5c
PN WO200250244-A2.
XX
XX
PD 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
PI
XX WPI; 2002-519880/55.
DR
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 93; 120pp; English.
PS
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
XX Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 GCGGAGCAAGATGGCGCAGA 120
Db 20 GCGGAGCAAGATGGCGCAGA 1
RESULT 60
AAD40894/c
ID AAD40894 standard; DNA; 20 BP.
XX
XX AAD40894;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123675.
DE
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT

FT FT /*tag= a
FT /mod_base= OTHER
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
PN 1
XX /*tag= d
XX /mod_base= m5c
FT 4
FT /*tag= e
FT /mod_base= m5c
FT 6..7
FT /*tag= f
FT /mod_base= m5c
FT 9
FT /*tag= g
FT /mod_base= m5c
FT 12
FT /*tag= h
FT /mod_base= m5c
FT 15..20
FT /*tag= c
FT /mod_base= OTHER
FT 18
FT /note= "2'-methoxyethyl residues"
FT 18
FT /*tag= i
FT /mod_base= m5c
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
PI
XX WPI; 2002-519880/55.
DR
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 93; 120pp; English.
PS
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
XX Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 GCGGAGCAAGATGGCGCAGA 120
Db 20 GCGGAGCAAGATGGCGCAGA 1
RESULT 60
AAD40894/c
ID AAD40894 standard; DNA; 20 BP.
XX
XX AAD40894;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123675.
DE
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT

QY 283 AAGCCAATGCTGAGGAGATG 302
 Db 20 AAGCCAATGCTGAGGAGATG 1

RESULT 61
 AAD40898/c
 ID AAD40898 standard; DNA; 20 BP.
 AC AAD40898;
 XX 30-OCT-2002 (first entry)
 DE Human HDAL antisense oligonucleotide ISIS #123679.
 XX Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 1
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 2
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 5
 FT /tag= f
 FT /mod_base= m5c
 FT modified_base 11
 FT /tag= g
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 16
 FT /tag= h
 FT /mod_base= m5c
 FT modified_base 20
 FT /tag= i
 FT /mod_base= m5c

XX WO200250244-A2.
 XX 27-JUN-2002.
 XX 07-DEC-2001; 2001WO-US046518.
 XX 19-DEC-2000; 2000US-0745167.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Wyatt JR;
 XX WPI; 2002-519880/55.
 XX Antisense compounds targeted against polynucleotides encoding Histone
 PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 PT infection.

PS Claim 3; Page 93; 120pp; English.
 XX The present invention relates to antisense compounds, compositions and
 CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
 CC Sequences of the invention are useful for inhibiting the expression of
 CC HDAL in cells or tissues and for treating an animal having a disease or
 CC condition associated with HDAL e.g., hyperproliferative condition, which
 CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
 CC resulting from a viral infection. Antisense compounds can be used as
 CC tools in differential and/or combinatorial analyses to elucidate the
 CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targeted to human
 CC HDAL DNA
 XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 405 GACTGTCAGTATTCGATGG 424
 Db 20 GACTGTCAGTATTCGATGG 1

RESULT 62
 AAD40919/c
 ID AAD40919 standard; DNA; 20 BP.
 AC AAD40919;
 XX 30-OCT-2002 (first entry)
 DE Human HDAL antisense oligonucleotide ISIS #123700.
 XX Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 10
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 13..14
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl residues"
 FT modified_base 18..19
 FT /tag= f
 FT /mod_base= m5c

XX WO200250244-A2.
 XX 27-JUN-2002.

```

PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 918 CGGTAGGTTGCTCAACT 937
Db 20 CGGTAGGTTGCTCAACT 1
RESULT 63
AAd40889/c
ID AAd40889 standard; DNA; 20 BP.
XX
AC AAd40889;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123670.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 6..7
FT /tag= d
FT /mod_base= m5c
FT

```

```

FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= e
FT /mod_base= m5c
FT modified_base 20
FT /tag= f
FT /mod_base= m5c
XX
WO200250244-A2.
PN
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 233 GCTGCTCAACTATGCTCT 252
Db 20 GCTGCTCAACTATGCTCT 1
RESULT 64
AAd40921/c
ID AAd40921 standard; DNA; 20 BP.
XX
AC AAd40921;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAl antisense oligonucleotide ISIS #123702.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX

```

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 947 AGGACACGCCAAGTGTGTGG 966
DB 20 AGGACACGCCAAGTGTGTGG 1

RESULT 65
AAD40899/c
ID RAD40899 standard; DNA; 20 BP.
XX
AC AAD40899;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAL antisense oligonucleotide ISIS #123580.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT modified_base 1
FT /note= "2'-methoxyethyl residues"
FT /tag= d
FT /mod_base= m5C
FT modified_base 4
FT /tag= e
FT /mod_base= m5C
FT modified_base 8
FT /tag= f
FT /mod_base= m5C
FT modified_base 13
FT /tag= g
FT /mod_base= m5C
FT modified_base 15
FT /tag= h
FT /mod_base= m5C
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT modified_base 19
FT /note= "2'-methoxyethyl residues"
FT /tag= i
FT /mod_base= m5C
XX
WO200250244-A2.
27-JUN-2002.
07-DEC-2001; 2001WO-US046518.
19-DEC-2000; 2000US-00745167.
(ISIS-) ISIS PHARM INC.
Monia BP, Wyatt JR;
WPI; 2002-519880/55.

Homo sapiens.
Synthetic.
Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1..2
FT /tag= d
FT /mod_base= m5C
FT modified_base 4
FT /tag= e
FT /mod_base= m5C
FT modified_base 6
FT /tag= f
FT /mod_base= m5C
FT modified_base 8
FT /tag= g
FT /mod_base= m5C
FT modified_base 13
FT /tag= i
FT /mod_base= m5C
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 18..19
FT /tag= j
FT /mod_base= m5C
XX
WO200250244-A2.
27-JUN-2002.
07-DEC-2001; 2001WO-US046518.
19-DEC-2000; 2000US-00745167.
(ISIS-) ISIS PHARM INC.
Monia BP, Wyatt JR;
WPI; 2002-519880/55.
Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions; e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.
Claim 3; Page 94; 120pp; English.
The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAL). Sequences of the invention are useful for inhibiting the expression of HDAL in cells or tissues and for treating an animal having a disease or condition associated with HDAL e.g., hyperproliferative condition, which is cancer of hematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targeted to human HDAL DNA
Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other: SQ

FT Antisense compounds targeted against polynucleotides encoding Histone
 FT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 FT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 FT infection.
 XX
 XX
 XX Claim 3; Page 93; 120pp; English.
 PS
 CC The present invention relates to antisense compounds, compositions and
 CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
 CC Sequences of the invention are useful for inhibiting the expression of
 CC HDAL in cells or tissues and for treating an animal having a disease or
 CC condition associated with HDAL e.g., hyperproliferative condition, which
 CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
 CC resulting from a viral infection. Antisense compounds either alone or in
 CC combination with other antisense compounds or therapeutics can be used as
 CC tools in differential and/or combinatorial analyses to elucidate the
 CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targeted to human
 CC HDAL DNA
 XX
 SQ Sequence 20 BP; 10 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 427 TGGTTGAGTTCTGTCAGTTG 446
 Db 20 TGGTTGAGTTCTGTCAGTTG 1
 RESULT 66
 AAD40906/c
 ID AAD40906 standard; DNA; 20 BP.
 AC
 AC AAD40906;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAL antisense oligonucleotide ISIS #123687.
 XX
 KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT modified_base 2..3
 FT /tag= d
 FT /mod_base= m5c
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT modified_base 17..18
 FT /tag= e
 FT /mod_base= m5c
 FT modified_base 20
 FT /tag= f
 FT /mod_base= m5c

XX WO200250244-A2.
 PN
 XX
 PD 27-JUN-2002.
 XX
 XX 07-DEC-2001; 2001WO-US046518.
 XX
 PR 19-DEC-2000; 2000US-00745167.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Wyatt JR;
 XX
 DR WPI; 2002-519880/55.
 XX
 XX Antisense compounds targeted against polynucleotides encoding Histone
 XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 XX infection.
 XX
 PS Claim 3; Page 93; 120pp; English.
 XX
 CC The present invention relates to antisense compounds, compositions and
 CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
 CC Sequences of the invention are useful for inhibiting the expression of
 CC HDAL in cells or tissues and for treating an animal having a disease or
 CC condition associated with HDAL e.g., hyperproliferative condition, which
 CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
 CC resulting from a viral infection. Antisense compounds either alone or in
 CC combination with other antisense compounds or therapeutics can be used as
 CC tools in differential and/or combinatorial analyses to elucidate the
 CC expression patterns of a portion or the entire complement of genes
 CC expressed within cells and tissues. They are commonly used as research
 CC reagents and diagnostics. They may also be useful prophylactically such
 CC as to prevent or delay infection, inflammation or tumour formation. The
 CC present DNA sequence is an antisense oligonucleotide targeted to human
 CC HDAL DNA
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 663 GAGGCTTCTACACACCGGA 682
 Db 20 GAGGCTTCTACACACCGGA 1
 RESULT 67
 AAD40911/c
 ID AAD40911 standard; DNA; 20 BP.
 AC
 AC AAD40911;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HDAL antisense oligonucleotide ISIS #123692.
 XX
 KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
 KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
 KW tumour; antisense; cytostatic; virucide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT modified_base 1..5
 FT /tag= b

FT FT /mod_base= OTHER
FT FT /note= "2'-methoxyethyl residues"
FT modified_base 9
FT FT /*tag= d
FT FT /mod_base= m5c
FT modified_base 12
FT FT /*tag= e
FT FT /mod_base= m5c
FT modified_base 16...20
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "2'-methoxyethyl residues"
FT modified_base 19
FT FT /*tag= f
FT FT /mod_base= m5c

XX WO200250244-A2.
XX PN
XX PP
XX PD 27-JUN-2002.
XX XX
XX PF 07-DEC-2001; 2001WO-US046518.
XX PF
XX PP 19-DEC-2000; 2000US-00745167.
XX PP (ISIS-) ISIS PHARM INC.
XX PA Monia BP, Wyatt JR;
XX PI WPI; 2002-519880/55.
XX DR
XX XX
XX PPT Antisense compounds targeted against polynucleotides encoding Histone deacetylase 1 useful for treating hyperproliferative conditions, e.g. cancer of hematopoietic, lymphoid, myeloid or breast, or a viral infection.

XX PT
XX PT
XX PPS Claim 3; Page 93; 120pp; English.

CC The present invention relates to antisense compounds, compositions and methods for modulating the expression of Histone deacetylase 1 (HDAL). Sequences of the invention are useful for inhibiting the expression of HDAL in cells or tissues and for treating an animal having a disease or condition associated with HDAL e.g., hyperproliferative condition, which is cancer of haematopoietic, lymphoid, myeloid or breast or a condition resulting from a viral infection. Antisense compounds either alone or in combination with other antisense compounds or therapeutics can be used as tools in differential and/or combinatorial analyses to elucidate the expression patterns of a portion or the entire complement of genes expressed within cells and tissues. They are commonly used as research reagents and diagnostics. They may also be useful prophylactically such as to prevent or delay infection, inflammation or tumour formation. The present DNA sequence is an antisense oligonucleotide targeted to human HDAL DNA

XX SQ Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

Best Match 1.2%; Score 20; DB 1; Length 20;
Query Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 769 AGTATTATGCTGTAACTAC 788
|||||
DB 20 AGTATTATGCTGTAACTAC 1

RESULT 68
AAD40888/c
ID AAD40888 standard; DNA; 20 BP.
XX AC
XX AC AAD40888;
XX AC
XX DT 30-OCT-2002 (first entry)
XX DE Human HDAL antisense oligonucleotide IGIS #123669.

QY 228 AATTGGCTGCTCAACTATGG 247
Db 20 AATTGGCTGCTCAACTATGG 1

RESULT 69
AAD40896/c
ID AAD40896 standard; DNA; 20 BP.
XX
AC AAD40896;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAL antisense oligonucleotide ISIS #123677.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophyllactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
modified_base 1..20
/tag= a
/mod_base= OTHER
modified_base 1..5
/tag= b
/mod_base= OTHER
/note= "Phosphorothioate backbone"
modified_base 5
/tag= d
/mod_base= m5c
modified_base 11
/tag= e
/mod_base= m5c
modified_base 14
/tag= f
/mod_base= m5c
modified_base 16..20
/tag= c
/mod_base= OTHER
modified_base 16..17
/tag= g
/mod_base= m5c
modified_base 19
/tag= h
/mod_base= m5c

WO200250244-A2.
27-JUN-2002.
07-DEC-2001; 2001WO-US046518.
19-DEC-2000; 2000US-00745167.
(ISIS-) ISIS PHARM INC.
Monia BP, Wyatt JR;
WPI; 2002-519880/55.
Antisense compounds targeted against polynucleotides encoding Histone
deacetylase 1 useful for treating hyperproliferative conditions, e.g.
cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
infection.

Claim 3; Page 93; 120pp; English.

CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 293 TGAGGAGATGACCAAGTACC 312
Db 20 TGAGGAGATGACCAAGTACC 1

RESULT 70
AAD40915/c
ID AAD40915 standard; DNA; 20 BP.
XX
AC AAD40915;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAL antisense oligonucleotide ISIS #123696.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophyllactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
modified_base 1..20
/tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
modified_base 1..5
/tag= b
/mod_base= OTHER
modified_base 2
/tag= d
/mod_base= m5c
modified_base 5
/tag= e
/mod_base= m5c
modified_base 7..8
/tag= f
/mod_base= m5c
modified_base 13
/tag= g
/mod_base= m5c
modified_base 16..20
/tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl residues"
modified_base 20
/tag= h
/mod_base= m5c

PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Wyatt JR;
PI
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 845 GTCCAAAGTAATCGAGATGT 864
Db 20 GTCCAAAGTAATCGAGATGT 1
RESULT 71
AAD40924/c
ID AAD40924 standard; DNA; 20 BP.
XX
AC AAD40924;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAL antisense oligonucleotide ISIS #123705.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT

FT modified_base 6
FT /*tag= d
FT /mod_base= m5c
FT modified_base 15
FT /*tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Wyatt JR;
PI
XX WPI; 2002-519880/55.
DR
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 6 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1099 ACAATGACTACTTTGAATAC 1118
Db 20 ACAATGACTACTTTGAATAC 1
RESULT 72
AAD40914/c
ID AAD40914 standard; DNA; 20 BP.
XX
AC AAD40914;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human HDAL antisense oligonucleotide ISIS #123695.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.


```
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FH Location/Qualifiers
XX FT modified_base
XX FT 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX FT modified_base
XX FT 1..5
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residues"
XX FT modified_base
XX FT 2..3
XX FT /tag= d
XX FT /mod_base= m5c
XX FT modified_base
XX FT 8
XX FT /tag= e
XX FT /mod_base= m5c
XX FT modified_base
XX FT 15
XX FT /tag= f
XX FT /mod_base= m5c
XX FT modified_base
XX FT 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residues"
XX FT modified_base
XX FT 20
XX FT /tag= g
XX FT /mod_base= m5c
XX FT
XX PN WO200250244-A2.
XX XX
XX XX 27-JUN-2002.
XX XX
XX XX 07-DEC-2001; 2001WO-US046518.
XX XX
XX XX 19-DEC-2000; 2000US-00745167.
XX XX
XX XX (ISIS-) ISIS PHARM INC.
XX XX
XX XX Monia BP, Wyatt JR;
XX XX
XX XX WPI; 2002-519880/55.
XX XX
XX PT Antisense compounds targeted against polynucleotides encoding Histone
XX PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX PT infection.
XX PT
XX PS Claim 3; Page 94; 120pp; English.
XX CC
XX CC The present invention relates to antisense compounds, compositions and
XX CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX CC Sequences of the invention are useful for inhibiting the expression of
XX CC HDAl in cells or tissues and for treating an animal having a disease or
XX CC condition associated with HDAl e.g., hyperproliferative condition which
XX CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX CC resulting from a viral infection. Antisense compounds either alone or in
XX CC combination with other antisense compounds or therapeutics can be used as
XX CC tools in differential and/or combinatorial analyses to elucidate the
XX CC expression patterns of a portion or the entire complement of genes
XX CC expressed within cells and tissues. They are commonly used as research
XX CC reagents and diagnostics. They may also be useful prophylactically such
XX CC as to prevent or delay infection, inflammation or tumor formation. The
XX CC present DNA sequence is an antisense oligonucleotide targeted to human
XX CC HDAl DNA
XX SQ
XX SQ Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1..2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 840 GTCATGTCACAAAGTAATGGA 859
DB |||||
20 GTCATGTCACAAAGTAATGGA 1

RESULT 73
AAD40930/C
ID AAD40930 standard; DNA; 20 BP.
XX AC AAD40930;
XX 30-OCT-2002 (first entry)
XX Human HDAl antisense oligonucleotide ISIS #123711.
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
XX Synthetic.
XX Key
XX Location/Qualifiers
XX FT modified_base
XX FT 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX FT modified_base
XX FT 1..5
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residues"
XX FT modified_base
XX FT 3
XX FT /tag= d
XX FT /mod_base= m5c
XX FT modified_base
XX FT 5
XX FT /tag= e
XX FT /mod_base= m5c
XX FT modified_base
XX FT 8..9
XX FT /tag= f
XX FT /mod_base= m5c
XX FT modified_base
XX FT 11
XX FT /tag= g
XX FT /mod_base= m5c
XX FT modified_base
XX FT 13
XX FT /tag= h
XX FT /mod_base= m5c
XX FT modified_base
XX FT 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl residues"
XX FT modified_base
XX FT 17
XX FT /tag= i
XX FT /mod_base= m5c
XX PN WO200250244-A2.
XX XX
XX XX 27-JUN-2002.
XX XX
XX XX 07-DEC-2001; 2001WO-US046518.
XX XX
XX XX 19-DEC-2000; 2000US-00745167.
XX XX
XX XX (ISIS-) ISIS PHARM INC.
XX XX
XX XX Monia BP, Wyatt JR;
XX XX
XX XX WPI; 2002-519880/55.
XX XX
XX PT Antisense compounds targeted against polynucleotides encoding Histone
XX PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX PT infection.
```

```

FT XX /mod_base= m5c
FN WO200250244-A2.
PD XX
PF 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX PF
XX 19-DEC-2000; 2000US-00745167.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Monia BP, Wyatt JR;
XX PI
XX WPI; 2002-519880/55.
XX DR
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions. e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Example 15; Page 94; 120pp; English.
XX PS
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAl DNA
XX
XX Sequence 20 BP; 0 A; 7 C; 3 G; 10 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1499 GAAACCAAGGAGGAGAGC 1518
Db |||||
20 GAAACCAAGGAGGAGAGC 1
RESULT 75
AAD40907/c
ID AAD40907 standard; DNA; 20 BP.
XX
XX AAD40907;
XX AC
XX AC
XX DT 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123688.
DE
DE Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1...20
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "phosphorothioate backbone"
FT modified_base 1..5

```


CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA

XX Sequence 20 BP; 1 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
SQ

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 AGGACGAGACGACCTGAC 1316
Db 20 AGGACGAGACGACCTGAC 1

RESULT 77
AAD40936/c
ID AAD40936 standard; DNA; 20 BP.
XX AAD40936;
AC
XX 30-OCT-2002 (first entry)
DT
XX Human HDAl antisense oligonucleotide ISIS #123717.
DE
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 1..4
FT /*tag= d
FT /mod_base= m5c
FT modified_base 10
FT /*tag= e
FT /mod_base= m5c
FT modified_base 13
FT /*tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /*tag= g
FT /mod_base= m5c
FT modified_base 20
FT /*tag= h
FT /mod_base= m5c
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.
XX Antisense compounds targetted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX

SQ Sequence 20 BP; 0 A; 8 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1514 GAAGCCAGAGCCAAAGGGG 1533
Db 20 GAAGCCAGAGCCAAAGGGG 1

RESULT 78
AAD40905/c
ID AAD40905 standard; DNA; 20 BP.
XX AAD40905;
AC
XX 30-OCT-2002 (first entry)
DT
XX Human HDAl antisense oligonucleotide ISIS #123686.
DE
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 8..9
FT /*tag= d
FT /mod_base= m5c
FT modified_base 11
FT /*tag= e
FT /mod_base= m5c
FT modified_base 14..15
FT /*tag= f
FT /mod_base= m5c
FT modified_base 16..20

1308 GACCCCTGACCAAGCGCATCTC 1327
ov

Db 20 GACCTGACAAGGCATCTC 1

RESULT 80

AAAD40904/C

XX AAD40904 standard; DNA; 20 BP.

XX AAD40904;

XX 30-OCT-2002 (first entry)

XX Human HDAl antisense oligonucleotide ISIS #123685.

XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;

XX viral infection; prophylactic; inflammation; phosphorothioate backbone;

XX tumour; antisense; cytostatic; virucide; ss.

XX Homo sapiens.

XX Synthetic.

XX

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /*tag= b

FT /mod_base= m5C

FT modified_base 7..8

FT /*tag= e

FT /mod_base= m5C

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 16..17

FT /*tag= f

FT /mod_base= m5C

XX WO200250244-A2.

XX 27-JUN-2002.

XX 07-DEC-2001; 2001WO-US046518.

XX 19-DEC-2000; 2000US-00745167.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.

XX Antisense compounds targeted against polynucleotides encoding Histone

XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.

XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral

XX infection.

XX Claim 3; Page 93; 120pp; English.

XX The present invention relates to antisense compounds, compositions and

XX methods for modulating the expression of Histone deacetylase 1 (HDAl).

XX Sequences of the invention are useful for inhibiting the expression of

XX HDAl in cells or tissues and for treating an animal having a disease or

XX condition associated with HDAl e.g., hyperproliferative condition, which

XX is cancer of haematopoietic, lymphoid, myeloid or breast or a condition

XX resulting from a viral infection. Antisense compounds either alone or in

XX combination with other antisense compounds or therapeutics can be used as

XX tools in differential and/or combinatorial analyses to elucidate the

CC expression patterns of a portion or the entire complement of genes

CC expressed within cells and tissues. They are commonly used as research

CC reagents and diagnostics. They may also be useful prophylactically such

CC as to prevent or delay infection, inflammation or tumour formation. The

CC present DNA sequence is an antisense oligonucleotide targeted to human

CC HDAl DNA

XX

SQ Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 581 CTTGCCCATCTCGAAGTGC 600

Db 20 CTTGCCCATCTCGAAGTGC 1

RESULT 81

AAAD40917/C

ID AAD40917 standard; DNA; 20 BP.

XX AAD40917;

XX 30-OCT-2002 (first entry)

XX Human HDAl antisense oligonucleotide ISIS #123698.

XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;

XX viral infection; prophylactic; inflammation; phosphorothioate backbone;

XX tumour; antisense; cytostatic; virucide; ss.

XX Homo sapiens.

XX Synthetic.

XX

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 1

FT /*tag= d

FT /mod_base= m5C

FT modified_base 3

FT /*tag= e

FT /mod_base= m5C

FT modified_base 5

FT /*tag= f

FT /mod_base= m5C

FT modified_base 10

FT /*tag= g

FT /mod_base= m5C

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 16

FT /*tag= h

FT /mod_base= m5C

FT modified_base 19

FT /*tag= i

FT /mod_base= m5C

XX WO200250244-A2.

XX 27-JUN-2002.

XX 07-DEC-2001; 2001WO-US046518.

XX

PR 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 94; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 AGATGTTCCAGCTAGTCG 878
Db 20 AGATGTTCCAGCTAGTCG 1

RESULT 82
AAD40923/c
ID AAD40923 standard; DNA; 20 BP.
XX
XX AAD40923;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAL antisense oligonucleotide ISIS #123704.
DE Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 5..6
FT /tag= d
FT /mod_base= m5c
FT modified_base 11..12
FT /tag= e

FT modified_base 14
FT /tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= g
FT /mod_base= m5c
XX
PN WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX Claim 3; Page 94; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1056 ACAGCTGTGGCCTGGATAC 1075
Db 20 ACAGCTGTGGCCTGGATAC 1

RESULT 83
AAD40909/c
ID AAD40909 standard; DNA; 20 BP.
XX
XX AAD40909;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAL antisense oligonucleotide ISIS #123690.
DE Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
KW

XX OS Homo sapiens.
 XX OS Synthetic.
 XX Key
 XX modified_base
 XX 1..20
 XX /tag= a
 XX /mod_base= OTHER
 XX /note= "Phosphorothioate backbone"
 XX modified_base
 XX 1..5
 XX /tag= b
 XX /mod_base= OTHER
 XX /note= "2'-methoxyethyl residues"
 XX modified_base
 XX 6..9
 XX /tag= d
 XX /mod_base= m5c
 XX modified_base
 XX 14..15
 XX /tag= e
 XX /mod_base= m5c
 XX modified_base
 XX 16..20
 XX /tag= c
 XX /mod_base= OTHER
 XX /note= "2'-methoxyethyl residues"
 XX WO200250244-A2.
 XX 27-JUN-2002.
 XX 07-DEC-2001; 2001WO-US046518.
 XX 19-DEC-2000; 2000US-00745167.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Wyatt JR;
 XX WPI; 2002-519880/55.
 XX Antisense compounds targeted against polynucleotides encoding Histone
 XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 XX infection.
 XX Claim 3; Page 93; 120pp; English.
 XX The present invention relates to antisense compounds, compositions and
 XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
 XX Sequences of the invention are useful for inhibiting the expression of
 XX HDAl in cells or tissues and for treating an animal having a disease or
 XX condition associated with HDAl e.g., hyperproliferative condition, which
 XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
 XX resulting from a viral infection. Antisense compounds either alone or in
 XX combination with other antisense compounds or therapeutics can be used as
 XX tools in differential and/or combinatorial analyses to elucidate the
 XX expression patterns of a portion or the entire complement of genes
 XX expressed within cells and tissues. They are commonly used as research
 XX reagents and diagnostics. They may also be useful prophylactically such
 XX as to prevent or delay infection, inflammation or tumour formation. The
 XX present DNA sequence is an antisense oligonucleotide targeted to human
 XX HDAl DNA
 XX Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
 XX Query Match 1..28; Score 20; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 26;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 724 TCCAGGAAGTGGGGACCTA 743
 Db 20 TCCAGGAAGTGGGGACCTA 1

RESULT 84

AAD40931/C
 ID AAD40931 standard; DNA; 20 BP.
 XX AAD40931;
 XX 30-OCT-2002 (first entry)
 XX Human HDAl antisense oligonucleotide ISIS #123712.
 XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
 XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
 XX tumour; antisense; cytostatic; virucide; ss.
 XX Homo sapiens.
 XX Synthetic.
 XX Key
 XX modified_base
 XX 1..20
 XX /tag= a
 XX /mod_base= OTHER
 XX /note= "Phosphorothioate backbone"
 XX modified_base
 XX 1..5
 XX /tag= b
 XX /mod_base= OTHER
 XX /note= "2'-methoxyethyl residues"
 XX modified_base
 XX 1..4
 XX /tag= d
 XX /mod_base= m5c
 XX modified_base
 XX 6
 XX /tag= e
 XX /mod_base= m5c
 XX modified_base
 XX 8
 XX /tag= f
 XX /mod_base= m5c
 XX modified_base
 XX 9..10
 XX /tag= g
 XX /mod_base= m5c
 XX modified_base
 XX 12..13
 XX /tag= h
 XX /mod_base= m5c
 XX modified_base
 XX 15
 XX /tag= i
 XX /mod_base= m5c
 XX modified_base
 XX 16..20
 XX /tag= c
 XX /mod_base= OTHER
 XX /note= "2'-methoxyethyl residues"
 XX modified_base
 XX 18
 XX /tag= j
 XX /mod_base= m5c
 XX WO200250244-A2.
 XX 27-JUN-2002.
 XX 07-DEC-2001; 2001WO-US046518.
 XX 19-DEC-2000; 2000US-00745167.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Wyatt JR;
 XX WPI; 2002-519880/55.
 XX Antisense compounds targeted against polynucleotides encoding Histone
 XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
 XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
 XX infection.
 XX Claim 3; Page 94; 120pp; English.
 XX The present invention relates to antisense compounds, compositions and

CC methods for modulating the expression of Histone deacetylase 1 (HDAL).

CC Sequences of the invention are useful for inhibiting the expression of

CC HDAL in cells or tissues and for treating an animal having a disease or

CC condition associated with HDAL e.g., hyperproliferative condition, which

CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition

CC resulting from a viral infection. Antisense compounds either alone or in

CC combination with other antisense compounds or therapeutics can be used as

CC tools in differential and/or combinatorial analyses to elucidate the

CC expression patterns of a portion or the entire complement of genes

CC expressed within cells and tissues. They are commonly used as research

CC reagents and diagnostics. They may also be useful prophylactically such

CC as to prevent or delay infection, inflammation or tumour formation. The

CC present DNA sequence is an antisense oligonucleotide targetted to human

CC HDAL DNA

XX Sequence 20 BP; 1 A; 12 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1378 CTGAAGAGGAGGAGGAGG 1397

DB 20 CTGAAGAGGAGGAGGAGG 1

RESULT 85

AAD40891/c

ID AAD40891 standard; DNA; 20 BP.

AC AAD40891;

XX 30-OCT-2002 (first entry)

DT Human HDAL antisense oligonucleotide ISIS #123672.

DE Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;

KW viral infection; prophylactic; inflammation; phosphorothioate backbone;

KX tumour; antisense; cytostatic; virucide; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 7

FT /tag= d

FT /mod_base= m5c

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 16..17

FT /tag= e

FT /mod_base= m5c

XX WO200250244-A2.

XX 27-JUN-2002.

XX 07-DEC-2001; 2001WO-US046518.

XX 19-DEC-2000; 2000US-00745167.

XX (ISIS-) ISIS PHARM INC.

PI Monia BP, Wyatt JR;

XX WPI; 2002-519880/55.

XX Antisense compounds targeted against polynucleotides encoding Histone

PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.

PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral

PT infection.

XX Claim 3; Page 93; 120pp; English.

XX The present invention relates to antisense compounds, compositions and

CC methods for modulating the expression of Histone deacetylase 1 (HDAL).

CC Sequences of the invention are useful for inhibiting the expression of

CC HDAL in cells or tissues and for treating an animal having a disease or

CC condition associated with HDAL e.g., hyperproliferative condition, which

CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition

CC resulting from a viral infection. Antisense compounds either alone or in

CC combination with other antisense compounds or therapeutics can be used as

CC tools in differential and/or combinatorial analyses to elucidate the

CC expression patterns of a portion or the entire complement of genes

CC expressed within cells and tissues. They are commonly used as research

CC reagents and diagnostics. They may also be useful prophylactically such

CC as to prevent or delay infection, inflammation or tumour formation. The

CC present DNA sequence is an antisense oligonucleotide targetted to human

CC HDAL DNA

XX Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATGGTCTCTACCGAAAAAT 262

DB 20 TATGGTCTCTACCGAAAAAT 1

RESULT 86

AAD40900/c

ID AAD40900 standard; DNA; 20 BP.

AC AAD40900;

XX 30-OCT-2002 (first entry)

DT Human HDAL antisense oligonucleotide ISIS #123681.

DE Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;

KW viral infection; prophylactic; inflammation; phosphorothioate backbone;

KX tumour; antisense; cytostatic; virucide; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl residues"

FT modified_base 2..3

FT /tag= d

FT /mod_base= m5c

FT modified_base 6

FT /tag= e

FT /mod_base= m5c

FT modified_base 9

FT /tag= f

FT /mod_base= m5c

```
FT modified_base 12 /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAl DNA
XX
XX Sequence 20 BP; 3 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 480 CTTAATAAGCAGCAGACGGA 499
XX |||||
XX 20 CTTAATAAGCAGCAGACGGA 1
XX
XX RESULT 87
XX AAD40890/c
XX ID AAD40890 standard; DNA; 20 BP.
XX
XX AC AAD40890;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAl antisense oligonucleotide ISIS #123671.
XX
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
```

```
FT Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT modified_base 2
FT /tag= d
FT /mod_base= m5c
FT modified_base 11..12
FT /tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAl DNA
XX
XX Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 238 TCAACTATGGTCTCTACCGA 257
XX |||||
XX 20 TCAACTATGGTCTCTACCGA 1
XX
XX RESULT 88
XX AAD40916/c
XX ID AAD40916 standard; DNA; 20 BP.
XX
XX AC AAD40916;
```

XX 30-OCT-2002 (first entry)
XX Human HDAl antisense oligonucleotide ISIS #123697.
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER
XX modified_base 1
XX /note= "2'-methoxyethyl residues"
XX /tag= d
XX /mod_base= m5c
XX modified_base 7
XX /tag= e
XX /mod_base= m5c
XX modified_base 10
XX /tag= f
XX /mod_base= m5c
XX modified_base 12..13
XX /tag= g
XX /mod_base= m5c
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX modified_base 18
XX /note= "2'-methoxyethyl residues"
XX /tag= h
XX /mod_base= m5c
XX WO200250244-A2.
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX Claim 3; Page 94; 120pp; English.
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research

CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAl DNA
XX Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 850 AAGTAATGGAGATGTTCCAG 869
Db 20 AAGTAATGGAGATGTTCCAG 1
RESULT 89
AAD40922/c
ID AAD40922 standard; DNA; 20 BP.
XX AAD40922;
AC AAD40922;
XX 30-OCT-2002 (first entry)
DT Human HDAl antisense oligonucleotide ISIS #123703.
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER
XX modified_base 11..12
XX /note= "2'-methoxyethyl residues"
XX /tag= d
XX /mod_base= m5c
XX modified_base 14..15
XX /tag= e
XX /mod_base= m5c
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX modified_base 17..18
XX /note= "2'-methoxyethyl residues"
XX /tag= f
XX /mod_base= m5c
XX modified_base 20
XX /tag= g
XX /mod_base= m5c
XX WO200250244-A2.
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX

```

PT Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAL).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAL in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAL e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAL DNA
XX
SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1006 GAGCGGTGGTTACACATT 1025
DB 20 GAGCGGTGGTTACACATT 1
RESULT 90
AAD40895/c
ID AAD40895 standard; DNA; 20 BP.
AC AAD40895;
XX
XX 30-OCT-2002 (first entry)
DE Human HDAL antisense oligonucleotide ISIS #123676.
XX
KW Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 6
FT /tag= d
FT /mod_base= m5c
FT modified_base 9
FT /tag= e
FT /mod_base= m5c
FT modified_base 11..12
FT /tag= f
FT /mod_base= m5c
FT modified_base 14
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20

```

```

FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT modified_base 17
FT /tag= h
FT /mod_base= m5c
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAL).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAL in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAL e.g., hyperproliferative condition, which
XX is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAL DNA
XX
XX Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 288 AATGCTGAGGAGATGACCAA 307
DB 20 AATGCTGAGGAGATGACCAA 1
RESULT 91
AAD40901/c
ID AAD40901 standard; DNA; 20 BP.
XX
XX AAD40901;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAL antisense oligonucleotide ISIS #123682.
XX
XX Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers

```

```
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT modified_base 1
FT /note= "2'-methoxyethyl residues"
FT modified_base 7..8
FT /*tag= d
FT /mod_base= m5c
FT modified_base 11
FT /*tag= e
FT /mod_base= m5c
FT modified_base 14
FT /*tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /*tag= g
FT /mod_base= m5c
FT modified_base 17
FT /*tag= h
FT /mod_base= m5c
FT modified_base 17
FT /*tag= h
FT /mod_base= m5c
PN WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAL).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAL in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAL e.g., hyperproliferative condition, which
XX is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumor formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAL DNA
XX
SQ Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 485 TAAGCAGCAGACGGACATCG 504
|||||
```

```
Db 20 TAAGCAGCAGACGGACATCG 1
RESULT 92
AAD40903/c
ID AAD40903 standard; DNA; 20 BP.
XX
XX AAD40903;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAL antisense oligonucleotide ISIS #123684.
XX
XX Human; histone deacetylase 1; HDAL; enzyme; hyperproliferative condition;
XX viral infection; prophylactic; inflammation; phosphorothioate backbone;
XX tumour; antisense; cytostatic; virucide; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..5
XX /*tag= b
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl residues"
XX modified_base 2..13
XX /*tag= d
XX /mod_base= m5c
XX modified_base 11..12
XX /*tag= e
XX /mod_base= m5c
XX modified_base 16..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl residues"
XX modified_base 17
XX /*tag= f
XX /mod_base= m5c
XX
XX WO200250244-A2.
XX
XX 27-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046518.
XX
XX 19-DEC-2000; 2000US-00745167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Wyatt JR;
XX
XX WPI; 2002-519880/55.
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX
XX Claim 3; Page 93; 120pp; English.
XX
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAL).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAL in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAL e.g., hyperproliferative condition, which
XX is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
```

```
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 576 ATCGTCTTGGCCATCTCGA 595
Db 20 ATCGTCTTGGCCATCTCGA 1
RESULT 93
AAD40918/c
ID AAD40918 standard; DNA; 20 BP.
XX
AC AAD40918;
XX
DT 30-OCT-2002 (first entry)
DE Human HDAl antisense oligonucleotide ISIS #123699.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT modified_base 1
FT /note= "2'-methoxyethyl residues"
FT modified_base 5..16
FT /tag= d
FT /mod_base= m5c
FT modified_base 10..13
FT /tag= e
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= f
FT /mod_base= m5c
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
XX
PN WO200250244-A2.
XX
PD 27-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046518.
XX
PR 19-DEC-2000; 2000US-00745167.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt JR;
XX
DR WPI; 2002-519880/55.
XX
PT Antisense compounds targeted against polynucleotides encoding Histone
```

```
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 94; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAl).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAl in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAl e.g., hyperproliferative condition, which
CC is cancer of hematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targetted to human
CC HDAl DNA
XX
SQ Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 905 CCTATCTGGGATCGGTAG 924
Db 20 CCTATCTGGGATCGGTAG 1
RESULT 94
AAD40920/c
ID AAD40920 standard; DNA; 20 BP.
XX
AC AAD40920;
XX
DT 30-OCT-2002 (first entry)
DE Human HDAl antisense oligonucleotide ISIS #123701.
XX
KW Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT modified_base 1
FT /note= "2'-methoxyethyl residues"
FT modified_base 3
FT /tag= d
FT /mod_base= m5c
FT modified_base 8
FT /tag= e
FT /mod_base= m5c
FT modified_base 13..14
FT /tag= f
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
```

```
FT FT /mod_base= OTHER
XX XX /note= "2'-methoxyethyl residues"
PN WO200250244-A2.
XX 27-JUN-2002.
XX 07-DEC-2001; 2001WO-US046518.
XX 19-DEC-2000; 2000US-00745167.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Wyatt JR;
XX WPI; 2002-519880/55.
XX Antisense compounds targeted against polynucleotides encoding Histone
XX deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX infection.
XX Claim 3; Page 94; 120pp; English.
XX The present invention relates to antisense compounds, compositions and
XX methods for modulating the expression of Histone deacetylase 1 (HDAl).
XX Sequences of the invention are useful for inhibiting the expression of
XX HDAl in cells or tissues and for treating an animal having a disease or
XX condition associated with HDAl e.g., hyperproliferative condition, which
XX is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
XX resulting from a viral infection. Antisense compounds either alone or in
XX combination with other antisense compounds or therapeutics can be used as
XX tools in differential and/or combinatorial analyses to elucidate the
XX expression patterns of a portion or the entire complement of genes
XX expressed within cells and tissues. They are commonly used as research
XX reagents and diagnostics. They may also be useful prophylactically such
XX as to prevent or delay infection, inflammation or tumour formation. The
XX present DNA sequence is an antisense oligonucleotide targeted to human
XX HDAl DNA
XX Sequence 20 BP; 2 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 942 ATCAAAGGACACGCCAAGTG 961
DB 20 ATCAAAGGACACGCCAAGTG 1
RESULT 95
AAD40934/c
ID AAD40934 standard; DNA; 20 BP.
AC AAD40934;
AC AAD40934;
DT 30-OCT-2002 (first entry)
XX Human HDAl antisense oligonucleotide ISIS #123715.
XX Human; histone deacetylase 1; HDAl; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
PH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
```

```
ABV73074/c
ID ABV73074 standard; DNA; 20 BP.
XX
AC ABV73074;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human HDAC-1 mRNA inhibiting antisense oligo HDAC1 AS2.
XX
KW Histone deacetylase; HDAC-4; cytostatic; neoplastic; cell proliferation;
KW HDAC-1; human; cancer; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200269947-A2.
XX
PD 12-SEP-2002.
XX
PF 14-JAN-2002; 2002WO-IB002002.
XX
PR 12-JAN-2001; 2001US-0261522P.
PR 12-JAN-2001; 2001US-0261674P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Besterman JM, Bonfils C, Woo SH, Vaisburg A, Delorme D;
PI Fournel M, Lavoie R, Li Z;
XX
DR WPI; 2002-750436/81.
XX
PT Inhibition of HDAC-4 activity in a cell useful for treating e.g. cancer
PT involves contacting the cell with an antisense oligonucleotide or a small
PT molecule inhibitor of HDAC-4.
XX
PS Disclosure; Page 32; 124pp; English.
XX
CC The invention relates to inhibition of histone deacetylase (HDAC)-4
CC activity in a cell that involves contacting the cell with an antisense
CC oligonucleotide complementary to a region of RNA encoding a portion of
CC HDAC-4 or a small molecule inhibitor of HDAC-4. The method is useful for
CC inhibiting neoplastic cell proliferation in an animal (preferably human)
CC and for treating cancer. Sequences ABV73073-3091 represent HDAC isotype-
CC specific antisense and mismatch oligonucleotides
XX
SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
XX
PT Query Match 1.2%; Score 20; DB 1; Length 20;
PT Best Local Similarity 100.0%; Pred. No. 26;
PT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
PS Disclosure; Page 32; 124pp; English.
XX
CC The invention relates to inhibition of histone deacetylase (HDAC)-4
CC activity in a cell that involves contacting the cell with an antisense
CC oligonucleotide complementary to a region of RNA encoding a portion of
CC HDAC-4 or a small molecule inhibitor of HDAC-4. The method is useful for
CC inhibiting neoplastic cell proliferation in an animal (preferably human)
CC and for treating cancer. Sequences ABV73073-3091 represent HDAC isotype-
CC specific antisense and mismatch oligonucleotides
XX
SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
XX
PT Query Match 1.2%; Score 20; DB 1; Length 20;
PT Best Local Similarity 100.0%; Pred. No. 26;
PT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1565 CCTCTCCAGCTCTGGCTTC 1584
DB 20 CCTCTCCAGCTCTGGCTTC 1
XX
RESULT 97
ABV73073/c
ID ABV73073 standard; DNA; 20 BP.
XX
AC ABV73073;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human HDAC-1 mRNA inhibiting antisense oligo HDAC1 AS1.
XX
KW Histone deacetylase; HDAC-4; cytostatic; neoplastic; cell proliferation;
KW HDAC-1; human; cancer; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200269947-A2.
XX
QY 1585 TCCTGAGTCCCTCAGTTTC 1604
DB 20 TCCTGAGTCCCTCAGTTTC 1
XX
RESULT 98
ABK87723/c
ID ABK87723 standard; DNA; 20 BP.
XX
AC ABK87723;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human histone deacetylase isoform 1 antisense oligonucleotide AS1.
XX
KW Human; ss; histone deacetylase; HDAC-1; cancer; cytostatic; antisense;
KW tumour suppressor; cell proliferation; tumour; programmed cell death;
KW necrotic cell death.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /tag= b
FT /mod_base= OTHER
FT /note= "These nucleotides have 2'-O-methyl groups
FT attached to their sugar residues"
FT modified_base 17..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "These nucleotides have 2'-O-methyl groups
FT attached to their sugar residues"
XX
PN US2002061860-A1.
```



```

XX PD 23-MAY-2002.
XX PF
XX PF 06-AUG-2001; 2001US-00817913.
XX PR
XX PR 24-MAR-2000; 2000US-0192157P.
XX PA (LIZZ/) LI Z.
XX PA (BONF/) BONFILS C.
XX PA (BEST/) BESTERMAN J.
XX PI
XX PI LI Z, Bonfils C, Besterman J;
XX WPI; 2002-507650/54.
XX DR
XX DR Agent that specifically inhibits an isoform of histone deacetylase,
XX PT useful for treating cancer and other cell proliferative diseases,
XX PT preferably comprises an antisense oligonucleotide.
XX PS
XX PS Claim 24; Page 6; 60pp; English.
XX CC
XX CC The invention relates to an agent that inhibits an isoform of histone
XX CC deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an antisense
XX CC oligonucleotide. Also included are inhibiting an HDAC isoform in a cell
XX CC by treatment with the agent, identifying an HDAC isoform that is required
XX CC for induction of cell proliferation or differentiation and inhibiting
XX CC cell proliferation by treatment with two antisense oligonucleotides or
XX CC small molecules that inhibit a specific HDAC isoform, or antisense
XX CC oligonucleotide or small molecules that inhibit DNA methyltransferase.
XX CC The agent therefore acts as a tumour suppressor. The agents are used to
XX CC treat diseases of cell proliferation and differentiation (e.g. cancer and
XX CC tumours), by inducing growth retardation, growth arrest or
XX CC programmed/necrotic cell death, specifically neoplastic cell
XX CC proliferation in humans. The agents are selective for particular
XX CC isoforms, compared to known inhibitors which are not selective. The
XX CC present sequence is an antisense oligonucleotide of the invention
XX CC targeting the polynucleotide which encodes the HDAC-1 isoform
XX SQ
XX SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1595 TGCTGAGTCCCTCACGTTTC 1604
DB 20 TGCTGAGTCCCTCACGTTTC 1
RESULT 99
ABK87724/C
ID ABK87724 standard; DNA; 20 BP.
XX AC ABK87724;
XX AC
XX DT 07-OCT-2002 (first entry)
XX DE
XX DE Human histone deacetylase isoform 1 antisense oligonucleotide AS2.
XX KW Human; ss; histone deacetylase; HDAC-1; cancer; cytostatic; antisense;
XX KW tumour suppressor; cell proliferation; tumour; programmed cell death;
XX KW necrotic cell death.
XX OS Homo sapiens.
XX
XX FH Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone"
XX FT modified_base 1..4
XX FT /*tag= b
XX FT /mod_base= OTHER

```

```

FT FT /note= "These nucleotides have 2'-O-methyl groups
FT FT attached to their sugar residues"
FT FT 17..20
FT FT /*tag= c
FT FT /mod_base= OTHER
FT FT /note= "These nucleotides have 2'-O-methyl groups
FT FT attached to their sugar residues"
XX PN US2002061860-A1.
XX PD
XX PD 23-MAY-2002.
XX PF
XX PF 06-AUG-2001; 2001US-00817913.
XX PR
XX PR 24-MAR-2000; 2000US-0192157P.
XX PA (LIZZ/) LI Z.
XX PA (BONF/) BONFILS C.
XX PA (BEST/) BESTERMAN J.
XX PI
XX PI LI Z, Bonfils C, Besterman J;
XX WPI; 2002-507650/54.
XX DR
XX DR Agent that specifically inhibits an isoform of histone deacetylase,
XX PT useful for treating cancer and other cell proliferative diseases,
XX PT preferably comprises an antisense oligonucleotide.
XX PS
XX PS Claim 24; Page 6; 60pp; English.
XX CC
XX CC The invention relates to an agent that inhibits an isoform of histone
XX CC deacetylase (HDAC-1 to HDAC-8) but not all isoforms, e.g. an antisense
XX CC oligonucleotide. Also included are inhibiting an HDAC isoform in a cell
XX CC by treatment with the agent, identifying an HDAC isoform that is required
XX CC for induction of cell proliferation or differentiation and inhibiting
XX CC cell proliferation by treatment with two antisense oligonucleotides or
XX CC small molecules that inhibit a specific HDAC isoform, or antisense
XX CC oligonucleotide or small molecules that inhibit DNA methyltransferase.
XX CC The agent therefore acts as a tumour suppressor. The agents are used to
XX CC treat diseases of cell proliferation and differentiation (e.g. cancer and
XX CC tumours), by inducing growth retardation, growth arrest or
XX CC programmed/necrotic cell death, specifically neoplastic cell
XX CC proliferation in humans. The agents are selective for particular
XX CC isoforms, compared to known inhibitors which are not selective. The
XX CC present sequence is an antisense oligonucleotide of the invention
XX CC targeting the polynucleotide which encodes the HDAC-1 isoform
XX SQ
XX SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
DB 20 CCTCTCCAGCTCTGGCTTCC 1
RESULT 100
ABZ76476/C
ID ABZ76476 standard; DNA; 20 BP.
XX AC ABZ76476;
XX AC
XX DT 23-JUN-2003 (first entry)
XX DE
XX DE Human HDAC1 mRNA targeting antisense oligo HDAC1 AS1.
XX KW HDAC; histone deacetylase; cytostatic; vasotrophic; antiproliferative;
XX KW antisense; ss.
XX OS Synthetic.
XX OS Homo sapiens.

```

XX WO2003024448-A2.
 XX 27-MAR-2003.
 XX 12-SEP-2002; 2002WO-US029017.
 XX 14-SEP-2001; 2001US-0322402P.
 XX 26-JUN-2002; 2002US-0391728P.
 XX (METH-) METHYLGENE INC.
 XX Delorme D, Woo SH, Vaisburg A, Moradel O, Leit S, Raeppe S;
 XX Frechette S, Bouchain G;
 XX WPI; 2003-342612/32.
 XX New histone deacetylase inhibitors, useful for treatment of proliferative
 XX diseases or conditions e.g. cancer.
 XX Disclosure; Page 72; 347pp; English.
 XX The invention relates to histone deacetylase inhibitors of specified
 XX formulae and their salts. The compounds inhibit histone deacetylase
 XX (HDAC) enzymatic activity. They can be used for treating cell
 XX proliferative diseases or condition (e.g. cancer, restenosis and
 XX psoriasis). Sequences ABZ76476-492 represent antisense and mismatch
 XX oligonucleotides targeting the 5' UTR (untranslated region) and 3' UTRs
 XX of the human HDAC1-8 genes
 XX Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 XX Query Match 1.2%; Score 20; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred.No. 26;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1585 TCGTCAGTCCCTCAGCTTC 1604
 XX 20 TCGTCAGTCCCTCAGCTTC 1
 XX
 XX RESULT 101
 XX ABZ76477/c
 XX ID ABZ76477 standard; DNA; 20 BP.
 XX AC ABZ76477;
 XX 23-JUN-2003 (first entry)
 XX Human HDAC1 mRNA targeting antisense oligo HDAC1 AS2.
 XX HDAC; histone deacetylase; cytosolic; vasotropic; antipsoriatic;
 XX antisense; ss.
 XX Synthetic.
 XX Homo sapiens.
 XX WO2003024448-A2.
 XX 27-MAR-2003.
 XX 12-SEP-2002; 2002WO-US029017.
 XX 14-SEP-2001; 2001US-0322402P.
 XX 26-JUN-2002; 2002US-0391728P.
 XX (METH-) METHYLGENE INC.
 XX Delorme D, Woo SH, Vaisburg A, Moradel O, Leit S, Raeppe S;
 XX Frechette S, Bouchain G;
 XX WPI; 2003-342612/32.

PT New histone deacetylase inhibitors, useful for treatment of proliferative
 XX diseases or conditions e.g. cancer.
 XX Disclosure; Page 72; 347pp; English.
 XX The invention relates to histone deacetylase inhibitors of specified
 XX formulae and their salts. The compounds inhibit histone deacetylase
 XX (HDAC) enzymatic activity. They can be used for treating cell
 XX proliferative diseases or condition (e.g. cancer, restenosis and
 XX psoriasis). Sequences ABZ76476-492 represent antisense and mismatch
 XX oligonucleotides targeting the 5' UTR (untranslated region) and 3' UTRs
 XX of the human HDAC1-8 genes
 XX Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;
 XX Query Match 1.2%; Score 20; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred.No. 26;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1565 CCTCTCCAGCTCTGGCTTC 1584
 XX 20 CCTCTCCAGCTCTGGCTTC 1
 XX
 XX RESULT 102
 XX ADC21703/c
 XX ID ADC21703 standard; DNA; 20 BP.
 XX AC ADC21703;
 XX 18-DEC-2003 (first entry)
 XX Human HDAC-1 antisense oligonucleotide AS1.
 XX HDAC; histone deacetylase; isoform; HDAC-1; HDAC-2; HDAC-3; HDAC-4;
 XX HDAC-5; HDAC-6; HDAC-7; HDAC-8; antisense gene therapy;
 XX cell proliferation; programmed cell death; necrotic cell death;
 XX neoplastic cell proliferation; cell differentiation; neoplasm; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX modified_base 1..20
 XX /tag= b
 XX /mod_base= OTHER
 XX /note= "Phosphorothioate backbone"
 XX modified_base 1..4
 XX /tag= a
 XX /mod_base= OTHER
 XX /note= "2'-O-methyl residues"
 XX modified_base 17..20
 XX /tag= c
 XX /mod_base= OTHER
 XX /note= "2'-O-methyl residues"
 XX US2002137162-A1.
 XX 26-SEP-2002.
 XX 26-MAR-2001; 2001US-00817538.
 XX 24-MAR-2000; 2000US-0192157P.
 XX 12-JAN-2001; 2001US-0261522P.
 XX (LIZZ/) LI Z
 XX (BONFI) BONFILS C.
 XX (BEST/) BESTERMAN J M.
 XX Li Z, Bonfils C, Besterman JM;
 XX WPI; 2003-786641/74.
 XX New antisense oligonucleotide that inhibits one or more specific histone

PT deacetylase isoforms, is useful in modulating cell proliferation
PT especially neoplasia.

PS Claim 7; SEQ ID NO 17; 52pp; English.

XX The invention relates to an antisense oligonucleotide comprising a
XX nucleotide sequence of 13 to 15 nucleotides that inhibits one or more
XX specific histone deacetylase isoforms (HDAC-1 to HDAC-8), where the
XX oligonucleotide is complementary to a region of RNA or double stranded
XX DNA. The oligonucleotide is useful in inhibiting one or more histone
XX deacetylases isoforms in a cell comprising contacting the cell with the
XX oligonucleotide. Cell proliferation is inhibited in the contacted cell
XX which undergoes growth retardation and growth arrest. The contacted cell
XX undergoes programmed and necrotic cell death. The oligonucleotide is also
XX useful in inhibiting neoplastic cell proliferation in an animal,
XX preferably a human. The oligonucleotide is also useful in identifying a
XX histone deacetylase isoform that is required for the induction of cell
XX proliferation comprising contacting the histone deacetylase isoform with
XX the oligonucleotide where a decrease in induction of cell proliferation
XX indicates that the isoform is required for the induction of cell
XX proliferation. The above method is also applicable to identifying
XX isoforms required for cell proliferation. The oligonucleotide is useful
XX in identifying an isoform required for the induction of cell
XX differentiation, where an induction of cell differentiation indicates
XX that the isoform is required for differentiation. Also useful in
XX modulating cell proliferation especially neoplasia. The present sequence
XX an antisense oligonucleotide directed against an HDAC isoform containing
XX mismatched bases.

SQ Sequence 20 BP; 7 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCTCAGTTTC 1604

Db 20 TGCTGAGTCCTCAGTTTC 1

RESULT 103

ID ADC21704/c

AC ADC21704;

XX 18-DEC-2003 (first entry)

DE Human HDAC-1 antisense oligonucleotide AS2.

XX Human; histone deacetylase; isoform; HDAC-1; HDAC-2; HDAC-3; HDAC-4;

KW HDAC-5; HDAC-6; HDAC-7; HDAC-8; antisense gene therapy;

KW cell proliferation; programmed cell death; necrotic cell death;

XX neoplastic cell proliferation; cell differentiation; neoplasia; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= b

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base 1..4

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-O-methyl residues"

FT modified_base 17..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-O-methyl residues"

PN US2002137162-A1.

XX

PD 26-SEP-2002.

XX 26-MAR-2001; 2001US-00817538.

XX 24-MAR-2000; 2000US-0192157P.

PR 12-JAN-2001; 2001US-0261522P.

XX (LIZZ/) LI Z.

PA (BONE/) BONFILS C.

PA (BEST/) BESTERMAN J M.

XX Li Z, Bonfils C, Besterman JM;

XX WPI; 2003-786641/74.

XX New antisense oligonucleotide that inhibits one or more specific histone
XX deacetylase isoforms, is useful in modulating cell proliferation.
XX especially neoplasia.

PS Claim 7; SEQ ID NO 18; 52pp; English.

XX The invention relates to an antisense oligonucleotide comprising a
XX nucleotide sequence of 13 to 15 nucleotides that inhibits one or more
XX specific histone deacetylase isoforms (HDAC-1 to HDAC-8), where the
XX oligonucleotide is complementary to a region of RNA or double stranded
XX DNA. The oligonucleotide is useful in inhibiting one or more histone
XX deacetylases isoforms in a cell comprising contacting the cell with the
XX oligonucleotide. Cell proliferation is inhibited in the contacted cell
XX which undergoes growth retardation and growth arrest. The contacted cell
XX undergoes programmed and necrotic cell death. The oligonucleotide is also
XX useful in inhibiting neoplastic cell proliferation in an animal,
XX preferably a human. The oligonucleotide is also useful in identifying a
XX histone deacetylase isoform that is required for the induction of cell
XX proliferation comprising contacting the histone deacetylase isoform with
XX the oligonucleotide where a decrease in induction of cell proliferation
XX indicates that the isoform is required for the induction of cell
XX proliferation. The above method is also applicable to identifying
XX isoforms required for cell proliferation. The oligonucleotide is useful
XX in identifying an isoform required for the induction of cell
XX differentiation, where an induction of cell differentiation indicates
XX that the isoform is required for differentiation. Also useful in
XX modulating cell proliferation especially neoplasia. The present sequence
XX an antisense oligonucleotide directed against an HDAC isoform containing
XX mismatched bases.

SQ Sequence 20 BP; 6 A; 3 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584

Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 104

ID AAS06923/c

XX AAS06923 standard; DNA; 24 BP.

XX AAS06923;

XX 11-SEP-2003 (revised)

DT 12-SEP-2001 (first entry)

XX HPIV1 HN gene PCR primer.

XX Infectious chimeric parainfluenza virus; antigenic determinant;

KW nucleocapsid phosphoprotein; large polymerase; attenuated vaccine;

KW human HPIV1; HPIV2; HPIV3; RSV; pathogen; measles; PCR primer;

KW respiratory syncytial virus; respiratory tract infection; ss.

XX Human parainfluenza virus 1.

OS

XX WO200142445-A2.
XX 14-JUN-2001.
XX
XX 08-DEC-2000; 2000WO-US033293.
XX
XX 10-DEC-1999; 99US-00458813.
XX 10-DEC-1999; 99US-00459062.
XX 10-DEC-1999; 99US-0170195P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Murphy BR, Collins PL, Schmidt AC, Durbin AP, Skiadopoulos MH,
XX Tao T;
XX
XX WPI; 2001-356173/37.
XX
XX Isolated infectious chimeric parainfluenza virus (PIV), useful in an
XX attenuated vaccine to elicit an immune response against one or more
XX virus(es) selected from human PIV1 (HPIV1), HPIV2 and HPIV3.
XX
XX Example 3; Page 112; 305pp; English.
XX
XX The present sequence for human PIV1 (HPIV1) HN gene PCR primer is used
XX with the HPIV1 F PCR primer (AA506922) in the construction of a HPIV3-
XX 1/HPIV2 HN gene chimera. Novel infectious chimeric parainfluenza viruses
XX (FIVs) comprise a major nucleocapsid protein (N), a nucleocapsid
XX phosphoprotein (P), a large polymerase protein (L), and a partial or
XX complete PIV vector background genome, or antigenome combined with one or
XX more heterologous gene(s) or genome segment(s) encoding one or more
XX antigenic determinants of one or more heterologous pathogen(s) to form a
XX chimeric genome or antigenome. The chimeric PIV is useful in an
XX attenuated vaccine to elicit an immune response against one or more
XX virus(es) selected from human PIV1 (HPIV1), HPIV2 and HPIV3. The chimeric
XX PIV may also elicit a polyspecific immune response against HPIV3, measles
XX or respiratory syncytial virus (RSV). An immunospecific composition may
XX also contain two chimeric PIVs, where the first chimeric PIV elicits an
XX immune response against HPIV3 and the second chimeric PIV elicits an
XX immune response against HPIV1 or HPIV2, and where both the first and
XX second chimeric PIVs elicit an immune response against the non-PIV
XX pathogen. Chimeric HPIV3, HPIV1 and HPIV2 are useful as vaccines to
XX prevent measles and upper or lower respiratory tract infections
XX particularly in young children. (Updated on 11-SEP-2003 to standardise OS
XX field)
XX
XX Sequence 24 BP; 6 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 633 ATTGATATTCACCATGGTGACGGC 656
Dy 24 ATTGCTATTCACCATGCAGACGGC 1

RESULT 105
AAA55797/c
ID AAA55797 standard; DNA; 20 BP.

XX AAA55797;
XX

XX 01-SEP-2000 (first entry)
XX

XX Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:40.
XX
XX Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
XX modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX antiinflammatory; inflammation; asthma; ss.

OS Homo sapiens.
XX WO200023112-A1.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024278.
XX 19-OCT-1998; 98US-0104804P.
XX (METH-) METHYLGENE INC.
XX
XX Besterman JM, Macleod AR, Siders WM;
XX WPI; 2000-339532/29.
XX
XX Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein
XX effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX of e.g. tumors.
XX
XX Disclosure; Page 29; 99pp; English.

XX The present invention describes a method for inhibiting the expression of
XX a gene in a cell comprising contacting the cell with an effective
XX synergistic amount of an antisense oligonucleotide which inhibits
XX expression of the gene, and an effective synergistic amount of a protein
XX effector of a product of the gene. Also described are: (1) a method for
XX treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX comprising an antisense oligonucleotide which inhibits expression of the
XX gene in operable association with a protein effector of a gene product;
XX and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX methods and compositions are useful as analytical tools for transgenic
XX studies and as therapeutic tools, e.g. as gene therapy tools for human
XX diseases including benign and malignant tumours, inflammation or asthma.
XX The methods, inhibitors and compositions of the invention that inhibit
XX expression or activity of a gene or gene product may be used to treat
XX patients having, or predisposed to developing, a disease responsive to
XX inhibition of the gene. These may also be used to activate silenced genes
XX to provide missing gene functions and improve a given condition.
XX Furthermore, the methods and compositions are useful as probes of the
XX physiological function of a gene product in an experimental cell culture
XX or animal system; and to evaluate the effect of inhibiting gene activity
XX or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
XX which are used in the exemplification of the present invention

XX Sequence 20 BP; 6 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CCTGAGCGCTCTGTCACTC 81
Dy 20 CCTGAGCGCTCTGTCACTC 1

RESULT 106
AAA55799/c

ID AAA55799 standard; DNA; 20 BP.

XX AAA55799;
XX

XX 01-SEP-2000 (first entry)
XX

XX Human histone deacetylase HD1 antisense oligonucleotide SEQ ID NO:42.
XX
XX Human; DNA methyltransferase; DNA Mefase; antisense oligonucleotide;
XX modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX antiinflammatory; inflammation; asthma; ss.

PT (benzenesulfonfylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
PT restenosis or fungal infections.
XX
PS Disclosure; Page 40; 147pp; English.
XX
CC The sequences given in AAH43102-14 are oligonucleotides which are
CC antisense to the histone deacetylase gene, HDAC-1. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to give an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1531 GGCTCAAGGAGGAGGCCAAG 1550
Db 20 GGCTCAAGGAGGAGGTCAAG 1
RESULT 109
AAD40902/C
ID AAD40902 standard; DNA; 20 BP.
AC AAD40902;
XX
XX 30-OCT-2002 (first entry)
XX Human HDAC1 antisense oligonucleotide ISIS #123693.
XX Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..20
FT /tag= b
FT /mod_base= m5c
FT modified_base 1
FT /note= "2'-methoxyethyl residues"
FT /mod_base= m5c
FT modified_base 3
FT /tag= e
FT /mod_base= m5c
FT modified_base 6
FT /tag= f
FT /mod_base= m5c
FT modified_base 12..13
FT /tag= g
FT /mod_base= m5c
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT modified_base 16
FT /note= "2'-methoxyethyl residues"
FT /tag= h
FT /mod_base= m5c
FT modified_base 19
FT /tag= i
FT /mod_base= m5c

XX WO200250244-A2.
PN
XX 27-JUN-2002.
FD
XX
XX 07-DEC-2001; 2001WO-US046518.
PF
XX 19-DEC-2000; 2000US-00745167.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Wyatt JR;
PI
XX WPI; 2002-519880/55.
DR
XX
XX Antisense compounds targeted against polynucleotides encoding Histone
PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
PT infection.
XX
PS Claim 3; Page 93; 120pp; English.
XX
CC The present invention relates to antisense compounds, compositions and
CC methods for modulating the expression of Histone deacetylase 1 (HDAC1).
CC Sequences of the invention are useful for inhibiting the expression of
CC HDAC1 in cells or tissues and for treating an animal having a disease or
CC condition associated with HDAC1 e.g.; hyperproliferative condition, which
CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
CC resulting from a viral infection. Antisense compounds either alone or in
CC combination with other antisense compounds or therapeutics can be used as
CC tools in differential and/or combinatorial analyses to elucidate the
CC expression patterns of a portion or the entire complement of genes
CC expressed within cells and tissues. They are commonly used as research
CC reagents and diagnostics. They may also be useful prophylactically such
CC as to prevent or delay infection, inflammation or tumour formation. The
CC present DNA sequence is an antisense oligonucleotide targeted to human
CC HDAC1 DNA
XX
SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 490 AGCAGACGGACATCGCGGTG 509
Db 20 AGCAGACGGACATCGCTGTG 1
RESULT 110
AAD40927/C
ID AAD40927 standard; DNA; 20 BP.
XX
XX AAD40927;
XX
XX 30-OCT-2002 (first entry)
XX
XX Human HDAC1 antisense oligonucleotide ISIS #123708.
XX Human; histone deacetylase 1; HDAC1; enzyme; hyperproliferative condition;
KW viral infection; prophylactic; inflammation; phosphorothioate backbone;
KW tumour; antisense; cytostatic; virucide; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..5
FT /tag= b

FT FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT 7
FT modified_base
FT /tag= d
FT /mod_base= m5C
FT 9
FT modified_base
FT /tag= e
FT /mod_base= m5C
FT 10
FT modified_base
FT /tag= f
FT /mod_base= m5C
FT 13
FT modified_base
FT /tag= g
FT /mod_base= m5C
FT 16..20
FT modified_base
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residues"
FT FT
XX WO200250244-A2.
XX PN
XX 27-JUN-2002.
XX PD
XX 07-DEC-2001; 2001WO-US046518.
XX PF
XX 19-DEC-2000; 2000US-00745167.
XX PR
XX (ISIS-) ISIS PHARM INC.
XX PA
XX Monia BP, Wyatt JR;
XX DI
XX WPI; 2002-519880/55.
XX DR
XX Antisense compounds targeted against polynucleotides encoding Histone
XX PT deacetylase 1 useful for treating hyperproliferative conditions, e.g.
XX PT cancer of hematopoietic, lymphoid, myeloid or breast, or a viral
XX PT infection.
XX PT
XX PS Claim 3; Page 94; 120pp; English.
XX PS
XX The present invention relates to antisense compounds, compositions and
XX CC methods for modulating the expression of Histone deacetylase 1 (HDAC1).
XX CC Sequences of the invention are useful for inhibiting the expression of
XX CC HDAC1 in cells or tissues and for treating an animal having a disease or
XX CC condition associated with HDAC1 e.g., hyperproliferative condition, which
XX CC is cancer of haematopoietic, lymphoid, myeloid or breast or a condition
XX CC resulting from a viral infection. Antisense compounds either alone or in
XX CC combination with other antisense compounds or therapeutics can be used as
XX CC tools in differential and/or combinatorial analyses to elucidate the
XX CC expression patterns of a portion or the entire complement of genes
XX CC expressed within cells and tissues. They are commonly used as research
XX CC reagents and diagnostics. They may also be useful prophylactically such
XX CC as to prevent or delay infection, inflammation or tumour formation. The
XX CC present DNA sequence is an antisense oligonucleotide targeted to human
XX CC HDAC1 DNA
XX SQ
Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1246 TCCAAACGACGCGATTCT 1265
DB 20 TCCAAATGACGCGATTCT 1
RESULT 111
ABT39526/c
ID ABT39526 standard; DNA; 17 BP.
XX AC
XX ABT39526;
XX DT

DT 12-JUN-2003 (first entry)
XX Tumour suppression related human fukutin oligo SEQ ID No 5163.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
OS
XX WO2003025175-A2.
XX PN
XX 27-MAR-2003.
XX PD
XX 17-SEP-2002; 2002WO-IB004208.
XX PF
XX 17-SEP-2001; 2001FR-00011978.
XX PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX PA
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
XX DR
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX Disclosure; Page 637; 720pp; French.
XX PS
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (antisense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX SQ
Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 902 CTCCTATCTGGGATC 918
DB 17 CTCCTATCTGGGATC 1
RESULT 112
ABT39292
ID ABT39292 standard; DNA; 17 BP.
XX AC
XX ABT39292;
XX DT 12-JUN-2003 (first entry)
XX

DE Tumour suppression related human fukutin oligo SEQ ID No 4929.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WC2003025175-A2.
XX
PD 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
PF
XX 17-SEP-2001; 2001FR-00011978.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
PA Teberman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-313353/30.
DR
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX Disclosure; Page 610; 720pp; French.
PS
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 2 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 915 GATCGTTAGTTCGTT 931
Db 1 GATCGTTAGTTCGTT 17
RESULT 113
AAV67421
ID AAV67421 standard; DNA; 21 BP.
XX
AC AAV67421;
XX
XX 21-DEC-1998 (first entry)
DT
XX Nucleotide fragment containing polymorphic site, WI-7310 (i).
DE
XX

KW ss; polymorphic site; nucleic acid analysis; diagnosis; monitoring;
KW cancer; inflammation; heart disease; CNS disease.
XX
OS Homo sapiens.
XX
PN WO9838846-A2.
XX
PD 11-SEP-1998.
XX
XX 06-MAR-1998; 98WO-US004571.
PF
XX 07-MAR-1997; 97US-00813159.
PR
XX 28-MAR-1997; 97US-0042125P.
PR
XX (AFFY-) AFFYMETRIX INC.
XX
XX Lipshutz RJ, Chee M, Fan J, Berno A;
PI
XX WPI; 1998-495419/42.
DR
XX New nucleic acid segments containing polymorphic sites, or complements
PT and methods of detecting a nucleic acid - for general use including
PT diagnosis and monitoring of diseases.
PT
XX Claim 1; Page 11; 42pp; English.
PS
XX New nucleic acid segment comprising one of the 10 - 100 bp sequences
CC given in the specification (sequences of a polymorphic site), or the
CC complement of the segment and a method of analysing a nucleic acid
CC comprising determining the base occupying the polymorphic site of the
CC polymorphic fragment sequences are disclosed in the specification. The
CC information obtained from nucleic acid analysis by the method described
CC is useful in diagnosis or monitoring of diseases like cancer,
CC inflammation, heart disease, CNS diseases, and susceptibility to
CC infection by microorganisms. In addition, the nucleic acid segments are
CC useful in manufacturing medication in the treatment of prophylaxis of
CC diseases, and also the use of the DNA segments as pharmaceutical
XX
SQ Sequence 21 BP; 9 A; 5 C; 6 G; 0 T; 0 U; 1 Other;
Query Match 1.1%; Score 17; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 69;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1480 AAGGAATCACCAGAGGA 1498
Db 3 AAGGAATCACCAGAGGA 21
RESULT 114
ABQ93091
ID ABQ93091 standard; DNA; 20 BP.
XX
AC ABQ93091;
XX
XX 29-AUG-2003 (revised)
DT
XX 21-OCT-2002 (first entry)
DT
XX T. tauschii/wheat D genome microsatellite cfa2226 left PCR primer.
DE
XX Microsatellite marker; wheat; D genome; mapping; genotyping;
KW polymorphism; phenotypic trait; QTL; quantitative trait locus;
KW disease-associated gene; development factor; quality factor;
KW resistance factor; wheat product; identification; detection;
KW genetically modified wheat; PCR; primer; ss.
XX
XX Regilops tauschii.
OS
XX Triticum aestivum.
OS
XX EP1217079-A1.
PN
XX 26-JUN-2002.
PD
XX

PF 22-DEC-2000; 2000EP-00403659.
PR 22-DEC-2000; 2000EP-00403659.
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX Bernard M, Sourdille P, Guyomarch H;
PI WPI; 2002-550410/59.
XX Map of wheat D genome comprising the genome location of a microsatellite
PT marker, useful for e.g. identifying genes responsible for a desired
PT phenotypic trait, especially quantitative trait loci in wheat, and
PT diseases.
XX
PS Claim 4; Page 10; 105pp; English.
XX
CC The invention relates to a map of the bread wheat D genome comprising the
CC genome location of a microsatellite marker selected from a group of 185
CC such markers (ABQ92733-ABQ92917). The invention also encompasses the use
CC of left (ABQ92918-ABQ93102) and right (ABQ93103-ABQ93287) primers to
CC amplify and detect the microsatellite markers, and to identify genes
CC responsible for a phenotypic trait of interest in wheat. Wheat is an
CC allohexaploid species consisting of 3 diploid genomes designated A, B and
CC D, resulting from two successive intercrossings involving at least three
CC different species. The D genome is thought to have been introduced in the
CC most recent intercrossing, between the amphiploid AABB and Triticum
CC tauschii (DD), probably involving only a limited number of genotypes of
CC wheat. Due to its polyploid genome, the large size of its genome,
CC and its low level of polymorphism, the genetic mapping of wheat has to
CC date been difficult. Microsatellites are tandemly repeated sequences
CC between one and six nucleotides long, and are very polymorphic in length,
CC mainly due to polymerase slippage during replication. This high degree of
CC polymorphism makes them especially suitable for the genetic mapping of
CC species which show little intraspecific polymorphism, such as wheat. In
CC addition, microsatellites are codominant, and exhibit Mendelian
CC inheritance. The 185 microsatellite markers of the invention are
CC developed from the ancestral diploid donor species Triticum tauschii and
CC map to the wheat D genome, which is less polymorphic than the A or B
CC genomes. These microsatellite markers thus help to overcome some of the
CC problems associated with the genetic mapping of wheat. The wheat D genome
CC map and the microsatellite markers and associated primers of the
CC invention are useful for identifying genes responsible for a phenotypic
CC trait of interest, most notably QTLs (quantitative trait loci). In
CC particular they may be used for analysing genes and alleles implicated in
CC disease and for identifying development factors, quality factors and
CC factors conferring resistance to pathogens and xenobiotics. The
CC microsatellite markers, and associated primers may be also be used in
CC mapping and genotyping diploid and polyploid species of Triticum,
CC particularly Aegilops, Triticum monococcum, Triticum durum, Triticum
CC aestivum, or related species; for identifying cultivars and hybrids of
CC Triticum and related species; to assess whether or not a product
CC comprises wheat or a related species; and to assess whether or not a
CC product comprises genetically modified wheat. The present sequence
CC represents a specifically claimed Triticum tauschii/wheat genome D
CC microsatellite marker left PCR primer of the invention. (Updated on 29-
CC AUG-2003 to standardise OS field)
XX
SQ Sequence 20 BP; 10 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1187 GGAGAAGATCAACAGCGAC 1206
DB 1 GGAGAAGATCAACAGCGAC 20
RESULT 115
AB292578/c
ID AB292578 standard; DNA; 20 BP.
XX

AC AB292578;
XX 17-OCT-2003 (first entry)
DT Human oligonucleotide sequence.
DE
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 7820; 872pp; English.
XX
XX The invention relates to a novel pharmacological composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Notes: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1179 GAGTACCTGGAGAAGATCAA 1198
DB 20 GAGGACCTGGAGAAGTTCAA 1
RESULT 116
ACC86770/c
ID ACC86770 standard; DNA; 20 BP.
XX

AC ACC86770;
 XX 04-AUG-2003 (first entry)
 XX Human VEGFR-1 chimeric phosphorothioate oligonucleotide SEQ ID NO:65.
 XX
 XX Vascular endothelial growth factor receptor 1; VEGF receptor; VEGFR;
 KW inhibitor; cytostatic; antirheumatic; antiarthritic; angiogenic;
 KW antiinflammatory; antisense gene therapy; hyperproliferative disorder;
 KW cancer; rheumatoid arthritis; angiogenesis; infection; inflammation;
 KW tumour formation; phosphorothioate; 2'-O-methoxyethyl; 2'-MOE; ss.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "This oligonucleotide has a phosphorothioate
 FT backbone and 2'-O-methoxyethyl (2'-MOE) wings at the 5'
 FT and 3' ends, which are 5 nucleotides in length. Also all
 FT cytidine residues are 5-methylcytidines"
 XX
 XX WO2003022227-A2.
 XX
 XX 20-MAR-2003.
 XX
 XX 12-SEP-2002; 2002WO-US029148.
 XX
 XX 13-SEP-2001; 2001US-00953318.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Watt AT;
 PI WPI; 2003-301004/29.
 XX
 XX New antisense oligonucleotide targeted to a nucleic acid encoding
 FT vascular endothelial growth factor receptor-1, useful for diagnosing or
 FT treating cancer, rheumatoid arthritis, or diseases or conditions
 FT involving angiogenesis.
 XX
 XX Claim 3; Page 83; 150pp; English.
 XX
 XX The present invention describes a compound (C) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding vascular endothelial growth
 CC factor receptor-1 (VEGFR-1), where the compound inhibits the expression
 CC of VEGFR-1 and specifically hybridises with the nucleic acid encoding
 CC VEGFR-1 or with an 8-nucleobase portion of an active site on the nucleic
 CC acid molecule encoding VEGFR-1. Also described: (1) a composition
 CC comprising (C) and a carrier or diluent; (2) inhibiting the expression of
 CC VEGFR-1 in cells or tissues by contacting the cells or tissues with (C)
 CC so that the expression of VEGFR-1 is inhibited; and (3) treating an
 CC animal having a disease or condition associated with VEGFR-1 by
 CC administering (C) to the animal so that the expression of VEGFR-1 is
 CC inhibited. (C) has antiangiogenic, antirheumatic, antiarthritic,
 CC cytostatic and antiinflammatory activities, and can be used in antisense
 CC gene therapy. The antisense compounds are useful for modulating the
 CC expression of VEGFR-1 and for treating diseases or conditions associated
 CC with the expression of VEGFR-1, such as hyperproliferative disorders
 CC (e.g. cancer), rheumatoid arthritis, or diseases or conditions involving
 CC angiogenesis. The antisense compounds are also useful for diagnostics,
 CC therapeutics, prophylaxis, e.g. to prevent or delay infection,
 CC inflammation or tumour formation, as research reagents and kits, and in
 CC distinguishing between functions of various members of a biological
 CC pathway. The present sequence represents a human VEGFR-2 chimeric
 CC phosphorothioate antisense oligonucleotide, which is used in an example
 XX from the present invention
 XX
 XX Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 67;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 518 TGGGGGCTGCACATGCAA 537
 DB 20 TGGGAGCTGCACCAAGCAA 1
 RESULT 117
 ACC44266/c
 ID ACC44266 standard; DNA; 20 BP.
 XX
 XX ACC44266;
 XX
 XX 07-JUL-2003 (first entry)
 XX
 XX 5' primer to amplify ribosomal protein S5 gene for ligand support method.
 DE Primer; ss; support; ligand immobilization; activated polyanion;
 KW DNA chip; protein chip; sugar chip; biosensor.
 KW
 XX Synthetic.
 OS
 XX WO2003027674-A1.
 XX
 XX 03-APR-2003.
 XX
 XX 20-SEP-2002; 2002WO-JP009661.
 XX
 XX 21-SEP-2001; 2001JP-00288149.
 XX
 XX (TAKA-) TAKARA BIO INC.
 XX
 XX Asada K, Imose N, Takeda O, Rokushima M, Kato I;
 PI WPI; 2003-342750/32.
 XX
 XX Polyanion-coated ligand immobilization support for production of DNA
 FT chips, protein chips and biosensors.
 XX
 XX Example 2; Page 37; 51pp; Japanese.
 XX
 XX The invention relates to a novel support for ligand immobilization, which
 CC is coated with a polyanion which has previously been activated. The
 CC support is useful for the production of DNA chips, protein chips, sugar
 CC chips and biosensors for investigative and diagnostic uses. Ligands which
 CC can be immobilized to the support include agonists, antagonists, toxins,
 CC venoms, virus epitopes, hormones, lectins, hormone receptors, peptides,
 CC nucleic acids, drugs, sugars, oligonucleotides, proteins, antigens,
 CC monoclonal antibodies, cells, viruses, and avidins. In an example of the
 CC invention, the ligand bound to the support is a PCR primer targeted to a
 CC number of genes and used to diagnose the presence and potentially the
 CC transcription of the genes. This sequence represents a 5' primer targeted
 CC to the ribosomal protein S5 gene
 XX
 XX Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 1.0%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 67;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 66 AGCGTCTCTGTCACCTCGGG 85
 DB 20 AGCGTCTCTGTCACCTCGGG 1
 RESULT 118
 ADD94313/c
 ID ADD94313 standard; DNA; 17 BP.
 XX
 XX ADD94313;
 XX
 XX 29-JAN-2004 (first entry)
 DT

XX Mouse HUI77/HUIV26 antibody related PCR primer SeqID198.
DE grafted antibody; complementarity determining region; CDR; light CDR;
XX heavy CDR; cryptic collagen epitope; solid tumour;
XX new blood vessel growth; angiogenesis; tumour growth; cytostatic;
XX collagen agonist; collagen antagonist; cancer metastasis;
XX anti-cryptic collagen; HUI77; HUIV26; mouse; murine; PCR; primer; ss;
XX heavy chain.
XX Mus musculus.
XX WO2003046204-A2.
XX 05-JUN-2003.
XX 26-NOV-2002; 2002WO-US038147.
XX 26-NOV-2001; 2001US-00995529.
XX 06-DEC-2001; 2001US-00011250.
XX (CELL-) CELL MATRIX INC.
XX Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX WPI; 2003-513649/48.
XX New cryptic collagen antibody with one or more complementarity
XX determining regions, useful for diagnosing and treating disorders
XX associated with angiogenesis, tumor growth and/or cancer metastasis.
XX Example 1; SEQ ID NO 198; 232pp; English.
XX This invention relates to a novel grafted antibody or its functional
XX fragment comprising one or more complementarity determining regions
XX (CDRs) of a defined light CDR and a heavy CDR with at least one amino
XX acid (aa) substitution where the antibody has specific binding activity
XX for a cryptic collagen epitope. The growth of all solid tumours requires
XX new blood vessel growth, angiogenesis, inhibition of which is an approach
XX to limiting tumour growth. The invention may allow development of
XX therapeutics with a cytostatic activity as a collagen agonist or
XX antagonist. The invention is useful for diagnosing and treating disorders
XX associated with angiogenesis, tumour growth and/or cancer metastasis. The
XX present sequence is that of a mutagenic PCR primer for amplification of
XX the sequence encoding the heavy chain of mouse HUI77 or HUIV26 antibodies
XX and used in the exemplification of the invention.
XX SQ Sequence 17 BP; 0 A; 3 C; 2 G; 11 T; 0 U; 1 Other;
Query Match 1.0%; Score 16.6; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 53;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1453 AAAAAGAGAAAGACCA 1469
DB 17 AAAAAGAGAAAGAYCCA 1
RESULT 119
AAAT27507/C
ID AAAT27507 standard; DNA; 20 BP.
XX AC AAAT27507;
XX 04-JUL-1996 (first entry)
XX Human c-raf kinase 3' untranslated region antisense oligonucleotide.
XX Antisense; anti-proliferative; tumour; cancer; raf; oncogene;
XX phosphorothioate; 2' sugar modification; psoriasis; restenosis; ss.
XX Synthetic.

XX Key Location/Qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "opt. phosphorothioate linked"
FT misc_feature 10..20
FT /*tag= b
FT /note= "contain 2'-O-methyl modifications"
XX WO9532987-A1.
XX 07-DEC-1995.
XX 31-MAY-1995; 95WO-US007111.
XX 31-MAY-1994; 94US-00250856.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Boggs RT;
XX WPI; 1996-030518/03.
XX Oligo(nucleotide(s) targetted to nucleic acids encoding human raf -
XX capable of inhibiting raf expression, used in treatment of
XX hyperproliferative disorders.
XX Claim 10; Page 18; 65pp; English.
XX AAT27481-727507 are human c-raf kinase antisense oligonucleotides used
XX for the inhibition of raf expression. The oligonucleotides (ONS) are
XX targeted to either coding region, start or stop signal or 5' or 3'
XX untranslated region (UTR) mRNA encoding human c-raf. The ONS may be
XX phosphorothioate linked and may contain modifications at the 2' position
XX of the sugar moiety. ONS are pref. complementary to either 3' or 5' UTRs,
XX phosphorothioate linked and contain 2'-O-alkyl sugar modifications. The
XX ONS are used to inhibit expression of human raf in partic. in conditions
XX associated with hyperproliferation e.g. cancer, restenosis, and psoriasis
XX SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1507 AGGAGGAGAGCCAGAG 1524
DB 19 AGGAGGAGAGCCAGAG 2
RESULT 120
AAAX36464/C
ID AAAX36464 standard; DNA; 20 BP.
XX AC AAAX36464;
XX 06-JUL-1999 (first entry)
XX Chimeric 2'-O-methyl oligo for c-raf inhibition.
XX RNaseH; RNA cleavage; DNA cleavage; hybridisation; protein kinase C gene;
XX gene expression modulation; raf; raf; therapy; AIDS; atherosclerosis;
XX infection; cell growth; ss.
XX Synthetic.
XX WO9730067-A1.
XX 21-AUG-1997.
XX 07-FEB-1997; 97WO-US002043.
XX 14-FEB-1996; 96US-0011620P.

(ISIS-) ISIS PHARM INC.
(NOVS) NOVARTIS AG.

Cook PB, Monia B, Altman K, Martin P;
WPI; 1997-424968/39.

Oligo:nucleotide with RNaseH activity, which specifically hybridises to DNA or RNA - comprises 1st and 2nd sub:sequence(s) having 2'-O-CH₂-CH₂-O-CH₃ and 2'-deoxy sugar moieties, useful for therapy or diagnosis.

Example 16; Page 41; 86pp; English.

This sequence is an example of an oligonucleotide of the invention, and is an inhibitor of c-rat expression. The invention relates to oligonucleotides (A), which specifically hybridises to RNA or DNA, comprises a linear sequence of nucleotide units linked by phosphodiester or phosphorothioate linkages, comprising a first subsequence having 2'-O-CH₂-CH₂-O-CH₃ sugar moieties and a second subsequence having 2'-deoxy sugar moieties. (A), which has RNaseH activity for cleaving a complementary strand, can be used to modulate the expression of ras, raf and protein kinase C genes, useful in the therapy of AIDS, atherosclerosis, bacterial or other infections, or to control aberrant cell growth in humans, animals or plants. (A) can also be used diagnostically, particularly when labelled to detect overexpression of mRNA or expression of abnormal RNA, including imaging of tissue sections, and as a research reagent. (A) has increased binding affinity for complementary strands attributable to the 2'-O-CH₂-CH₂-O-CH₃ sugar moiety, which overcomes the loss of affinity caused by altered intersugar links), and increased resistance to nuclease (from the modified links and the 2'-O-CH₂-CH₂-O-CH₃ sugar moiety)

Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. NO. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1507 AGGAGGAGGAAGCCAGAAG 1524
DB 19 AGGAGGAGGAAGCCAGCAG 2

RESULT 121
AAT59728/c
ID AAT59728 standard; DNA; 20 BP.
XX AAT59728;
XX
DT 06-OCT-1997 (first entry)
XX
XX Human raf inhibitor oligonucleotide ON21.
XX
XX
KW raf; inhibitor; antisense; liposome; cancer; abnormal expression;
KW anti-hyperproliferative; ss.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
FT modified_base 1...20
FT /tag= a
FT /note= "phosphorothioate backbone linkages"
FT modified_base 10..20
FT /tag= b
FT /note= "2' position of the sugar moiety is substituted by
XX methoxy"
XX
XX WO9704787-A1.
XX
XX 13-FEB-1997.
XX
XX 24-JUL-1996; 96WO-GB001775.
XX
XX

PA (CIBA) CIBA GEIGY AG.
 XX
 PI Nicklin PL, Steward A;
 XX
 DR WPI; 1997-202610/18.
 XX
 PT Composition for cancer treatment - comprising anionic polysaccharide, and
 XX oligo-nucleotide targetted to mRNA encoding human c-raf and dextran
 XX sulphate.
 XX
 PS Claim 16; Page 15; 21pp; English.
 XX
 CC A pharmaceutical composition has been developed comprising an
 CC oligonucleotide, targeted to human raf encoding mRNA, and an anionic
 CC polysaccharide. The present sequence represents a specifically claimed
 CC oligonucleotide for use in the composition. The composition can be used
 CC to treat mammalian cancer, especially human lung, stomach, renal, breast,
 CC laryngeal, pancreatic or colorectal cancer, or malignant melanoma. The
 CC anionic polysaccharide increases tumour uptake of the oligonucleotide,
 CC particularly an oligonucleotide targeted to human raf encoding mRNA
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGAG 2
 RESULT 123
 ID AAX15070/c
 AC AAX15070;
 XX
 DT 20-MAR-2003 (revised)
 DT 16-APR-1999 (first entry)
 XX
 DE c-raf antisense chimeric oligonucleotide of the invention.
 XX
 KW Nuclease resistant; ribofuranosyl moiety; 2'-aminoalkoxy; tumour;
 KW 2'-imidazolylalkoxy; modulation; activity; AIDS; atherosclerosis;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /note= "phosphorothioated"
 XX
 DN US5872232-A.
 XX
 PD 16-FEB-1999.
 XX
 XX 06-JUN-1995; 95US-00471973.
 XX
 PR 11-JAN-1990; 90US-00463358.
 PR 13-AUG-1990; 90US-00566977.
 PR 12-AUG-1991; 91WO-US005720.
 PR 05-MAR-1992; 92US-00835932.
 PR 01-JUL-1992; 92US-00854634.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Cook PD, Kawasaki AM;
 PI
 XX WPI; 1999-166721/14.
 DR
 XX New 2'-O-modified oligo-nucleotide (s) - comprising nucleotide(s)

PT comprising a 2'-aminoalkoxy or 2'-imidazolylalkoxy substituent, used for
 PT hybridisation to RNA or DNA.
 XX
 PS Example 31; Col 50; 48pp; English.
 XX
 CC The present oligonucleotide exemplifies the oligonucleotides of the
 CC invention. Oligonucleotides of the invention are nuclease resistant, and
 CC comprise covalently-bound nucleosides that individually include a ribose
 CC or deoxyribose sugar portion and base portion where the nucleosides are
 CC joined together by internucleoside linkages such that the base portion of
 CC the nucleosides form a mixed base sequence that is complementary to a RNA
 CC base sequence or to a DNA base sequence. At least one of the nucleosides
 CC has a modified ribofuranosyl moiety bearing a 2'-aminoalkoxy or 2'-
 CC imidazolylalkoxy substituent. The nuclease resistant compounds can be
 CC used for modulating the activity of DNA or RNA. They can be used for
 CC treating organisms having a disease characterised by the undesired
 CC production of a protein. Diverse organisms such as bacteria, yeast,
 CC protozoa, algae, plant and higher animal forms including warm-blooded
 CC animals can be treated in this manner. The compounds can be used for
 CC treating e.g. AIDS, atherosclerosis or tumours. They can also be used in
 CC diagnostic methods for detecting the presence or absence of abnormal RNA
 CC molecules, or abnormal or inappropriate expression of normal RNA
 CC molecules in organisms or cells. (Updated on 20-MAR-2003 to correct PR
 XX field.)
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGAG 2
 RESULT 124
 ID AAZ11537/c
 AC AAZ11537;
 XX
 DT 05-NOV-1999 (first entry)
 DE Human c-raf kinase antisense oligo ISIS # 7853.
 XX
 KW Human; raf; diagnosis; abnormal proliferative state; hyperproliferation;
 KW cancer; psoriasis; blood vessel restenosis; c-raf kinase; antisense; ss.
 XX
 OS Synthetic.
 XX
 OS Homo sapiens.
 XX
 PN US5952229-A.
 XX
 PD 14-SEP-1999.
 XX
 XX 26-NOV-1996; 96US-00756806.
 XX
 PR 31-MAY-1994; 94US-00250856.
 PR 31-MAY-1995; 95WO-US007111.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Boggs RT, Monia BP;
 XX
 DR WPI; 1999-527018/44.
 XX
 PT Oligonucleotides targeted to human raf mRNA useful for treating and
 PT diagnosing abnormal proliferative states and inhibiting raf expression.
 XX
 PS Claim 1; Col 11; 29pp; English.
 XX
 CC The invention provides antisense oligonucleotides targeted to mRNA

CC encoding human raf and capable of inhibiting raf expression. The
 CC antisense oligonucleotides are useful for treating and diagnosing
 CC abnormal proliferative states and hyperproliferation (e.g. cancer,
 CC psoriasis, or blood vessel restenosis), and inhibiting raf expression.
 CC Sequences AAZ1511-537 and AAZ11565-573 represent antisense
 CC oligonucleotides for human c-raf kinase
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGCAG 2
 RESULT 125
 ID AAX05468/c
 AC AAX05468;
 XX
 XX 20-APR-1999 (first entry)
 DT
 DE Chimeric antisense oligo for c-raf gene.
 XX
 XX Nuclease resistant; modified; deoxyfuranosyl moiety; therapy; infection;
 KW AIDS; atherosclerosis; tumour; c-raf; antisense; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /note= "contains phosphorothioate linkages; optional 2' O
 FT -methyl modification on some base pairs"
 XX
 XX US5859221-A.
 XX
 XX 12-JAN-1999.
 XX
 XX 06-JUN-1995; 95US-00468037.
 XX
 XX 11-JAN-1990; 90US-00463358.
 PR 13-AUG-1990; 90US-00566977.
 PR 12-AUG-1991; 91WO-US005720.
 PR 05-MAR-1992; 92US-00835932.
 PR 01-JUL-1992; 92US-00854634.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Cook PD, Kawasaki AM;
 XX
 XX WPI; 1999-120005/10.
 XX
 XX Nuclease resistant oligonucleotide analogues - having nucleosides
 PT including modified deoxyfuranosyl moiety bearing 2'-substituent to
 PT increase binding affinity.
 XX
 XX Example 31; Col 51; 49pp; English.
 PS
 XX The invention relates to a nuclease resistant compound that hybridises
 CC with RNA or DNA. The compound comprises covalently-bound nucleosides that
 CC individually include a ribose or deoxyribose sugar portion and a base
 CC portion, where the nucleosides are joined together by internucleoside
 CC linkages such that the base portion of the nucleosides form a mixed base
 CC sequence that is complementary to a RNA base sequence or to a DNA base
 CC sequence; and where at least 1 of the nucleosides includes a modified
 CC deoxyfuranosyl moiety bearing a 2'-substituent selected from cyano, and
 CC fluoromethyl, thioalkoxyl, alkylsulphonyl, alkylsulphonyl, allyloxy and

CC alkeneoxy groups. The nuclease resistant oligonucleotides (ONs) can bind
 CC to and modulate the activity of DNA or RNA and can be used for treating
 CC organisms having a disease characterised by the undesired production of a
 CC protein. They can be used in therapeutic or prophylactic treatment in
 CC organisms such as bacteria, yeast, protozoa, algae, plant and higher
 CC animal forms including warm-blooded animals. The ONs can also be used for
 CC treating infections, AIDS, atherosclerosis or tumours. The products can
 CC be used for detection and diagnosis. The ONs provide enhanced binding to
 CC targets. Increased binding of 2'-sugar modified sequence-specific ONs
 CC provides superior potency and specificity compared to phosphorus-modified
 CC ONs. The present sequence represents a chimeric antisense oligo for c-raf
 CC gene
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGCAG 2
 RESULT 126
 ID AAZ10296/c
 XX AAZ10296 standard; DNA; 20 BP.
 AC AAZ10296;
 XX
 XX 20-MAR-2003 (revised)
 DT 08-NOV-1999 (first entry)
 DT
 DE Oligonucleotide used to inhibit c-raf gene expression.
 XX
 XX Antisense oligonucleotide; c-raf; nuclease resistance;
 KW RNase H strand cleavage; phosphorothioate; oligonucleotide therapeutic;
 KW AIDS; atherosclerosis; ss.
 XX
 OS Synthetic.
 OS
 XX US5955589-A.
 XX
 XX 21-SEP-1999.
 XX
 XX 06-JUN-1995; 95US-00465880.
 XX
 XX 24-DEC-1991; 91US-00814961.
 PR 23-DEC-1992; 92WO-US011339.
 PR 21-JUN-1994; 94US-00244993.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Monia BP, Cook PD;
 XX
 XX WPI; 1999-539598/45.
 XX
 XX Oligonucleotides eliciting RNase H activity useful for diagnosis and
 PT treatment of diseases e.g AIDS or atherosclerosis.
 XX
 XX Example 14; Col 24; 34pp; English.
 PS
 XX The present sequence represents a phosphorothioate antisense
 CC oligonucleotide used to inhibit c-raf gene expression. The
 CC oligonucleotide is a gapped 2'-F (2'-H) nucleotides and the second part
 CC has at least two consecutive 2'-F (2'-H) nucleotides and the second part
 CC has at least five consecutive nucleotides with 2'-H sugar moieties. The
 CC modified oligonucleotide has increased nuclease resistance, and increased
 CC binding affinity for substrates. The oligonucleotide elicits RNase H
 CC strand cleavage of specific RNAs. Oligonucleotides of the invention are
 CC useful for the diagnosis, detection and treatment of conditions
 CC susceptible to oligonucleotide therapeutics (e.g. AIDS and
 CC atherosclerosis). (Updated on 20-MAR-2003 to correct PR field.)
 CC

XX Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGAG 2

RESULT 127
 AAZ48166/c
 ID AAZ48166 standard; DNA; 20 BP.
 AC AAZ48166;
 XX 14-MAR-2000 (first entry)
 DT
 DE C-raf chimeric phosphorothioate oligonucleotide SEQ ID NO:13.
 XX Polyribonucleotide solid phase synthesis; diagnosis; hybridisation;
 KW protein production modulation; 2'-deoxyfuranosyl moiety; anti-HIV;
 KW antiarteriosclerotic; nuclease resistant; atherosclerosis; AIDS;
 KW abnormal cell proliferation; tumour formation; ss.
 XX Synthetic.
 OS
 XX US6005087-A.
 PN
 XX
 PD 21-DEC-1999.
 XX
 XX 05-MAR-1998; 98US-00035357.
 XX
 XX 11-JAN-1990; 90US-00463358.
 XX
 PR 13-AUG-1990; 90US-00566977.
 PR 12-AUG-1991; 91WO-US005720.
 PR 05-MAR-1992; 92US-00835932.
 PR 01-JUL-1992; 92US-00854634.
 PR 06-JUN-1995; 95US-00468037.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX
 PI Kawasaki AM, Cook PD;
 XX
 XX WPI; 2000-072074/06.
 DR
 XX
 XX Nuclease resistant oligonucleotides useful as research agents, diagnostic
 PT agents, and in the treatment of atherosclerosis and AIDS.
 PT
 XX
 XX Example 31; Col 51; 49pp; English.

The present invention describes nuclease resistant oligonucleotides (I) comprising 2'-fluoro modified ribofuranosyl nucleotides. (I) comprise covalently bound nucleotides, where the nucleotides are joined together by: (a) internucleotide linkages such that the base portion of the nucleotides forms a mixed base sequence; and (b) at least one of the nucleotides includes a modified ribofuranosyl group bearing a 2'-fluoro substituent; provided that at least two of the nucleotides are 2'-fluoro modified ribofuranosyl nucleotides when the internucleotide linkages are phosphodiester nucleotides. (I) bind to their target mRNA and inhibit its expression. (I) are resistant to nuclease degradation and hybridise with appropriate strength and fidelity to its target RNA/DNA. (I) are also useful as research agents, diagnostic agents and as oligonucleotide therapeutics. (I) may be used to treat atherosclerosis following angioplasty to prevent reocclusion of the treated arteries. (I) may also be used in conjunction with ATR to treat AIDS patients. (I) have been used to modulate the expression of RAF gene, a cellular gene whose activate form has been implicated in abnormal cell proliferation and tumour formation. (I) are also used to modulate the expression of protein kinase C. (I) exhibit hybridisation properties of higher quality than phosphorous modified oligonucleotide duplexes containing

CC methylphosphonates, phosphoramidates and phosphate triesters. The present
 CC sequence represent an oligonucleotide used in the exemplification of the
 CC present invention
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 XX Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGAG 2

RESULT 128
 AAA73515/c
 ID AAA73515 standard; DNA; 20 BP.
 AC AAA73515;
 XX 28-NOV-2000 (first entry)
 DT
 DE C-raf kinase antisense oligonucleotide #36 (ISIS #7853).
 XX Human; c-raf; protein kinase; antisense oligonucleotide; cancer;
 KW signal transduction; hyperplasia; pulmonary fibrosis; angiogenesis;
 KW psoriasis; atherosclerosis; smooth muscle cell proliferation; stenosis;
 KW restenosis; inflammatory disorder; tissue graft rejection;
 KW endotoxin shock; glomerular nephritis; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "All or some nucleotides are optionally with 2'-
 methoxyethoxy modification. Also, optionally
 phosphodiester or phosphothioate backbone"
 FT
 XX US6090626-A.
 PN
 XX
 PD 18-JUL-2000.
 XX
 XX 28-AUG-1998; 98US-00143214.
 PF
 XX 31-MAY-1994; 94US-00250856.
 PR 31-MAY-1995; 95WO-US007111.
 PR 26-NOV-1996; 96US-00756806.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Boggis RT, Monia BP;
 PI
 XX WPI; 2000-531424/48.
 DR
 XX Antisense oligonucleotides targeted to nucleic acid molecule encoding
 PT human raf useful for diagnosis, treatment of raf-associated cell
 PT proliferative conditions such as cancer, psoriasis or blood vessel
 PT restenosis.
 PT
 XX Claim 31; Col 10; 31pp; English.
 PS
 XX C-raf is a serine-threonine-specific protein kinase and is thought to
 CC play a fundamental role in signal transduction, and cell proliferation
 CC control. The present sequence is an antisense oligonucleotide. This
 CC sequence is targeted to human c-raf gene, resulting in c-raf expression
 CC inhibition. The present sequence may be useful for treating and raf-
 CC associated cell hyperproliferation conditions such as cancer,
 CC hyperplasias, pulmonary fibrosis, angiogenesis, psoriasis,
 CC atherosclerosis and smooth muscle cell proliferation in blood vessels
 CC e.g. stenosis or restenosis following angioplasty. Also, the present

CC sequence may be useful for treating inflammatory disorders such as tissue
 CC graft rejection, endotoxin shock and glomerular nephritis
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGGAAG 1524
 Db 19 AGGAGGAGAGCCAGCAG 2
 RESULT 129
 AAD44740/c
 ID AAD44740 standard; DNA; 20 BP.
 XX
 AC AAD44740;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human c-raf kinase antisense oligonucleotide ISIS #7853.
 XX
 KW Human; raf; hyperproliferation; neovascularisation; ocular angiogenesis;
 KW therapy; cancer; cytostatic; anti-angiogenic; vascular; ophthalmological;
 KW antisense; phosphorothioate backbone; c-raf kinase; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /notes= "Phosphorothioate backbone"
 FT modified_base 10..20
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methyl nucleotides"
 XX
 PN US6410518-B1.
 XX
 PD 25-JUN-2002.
 XX
 XX 18-FEB-2000; 2000US-00506073.
 XX
 PR 31-MAY-1994; 94US-00250856.
 PR 31-MAY-1995; 95WO-US007111.
 PR 26-NOV-1996; 96US-00756806.
 PR 07-JUL-1997; 97US-00888982.
 PR 06-JUL-1998; 98WO-US013961.
 PR 28-AUG-1998; 98US-00143214.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP;
 XX
 DR WPI; 2002-597918/64.
 XX
 PT Treating cancer, angiogenesis or neovascularization by administering
 PT antisense oligonucleotides targeted to human raf sequences.
 XX
 PS Disclosure; Col 14; 41pp; English.
 XX
 CC The present invention relates to novel antisense oligonucleotides which
 CC are targeted to nucleic acids encoding human raf proteins and capable of
 CC inhibiting raf expression. The invention also relates to methods of
 CC inhibiting hyperproliferation of cells which involves contacting the
 CC hyperproliferating cells with a therapeutically effective amount of an
 CC oligonucleotide of the invention. The method is useful for treating
 CC cancer, angiogenesis or neovascularisation, especially ocular
 CC angiogenesis or neovascularisation. The present DNA sequence is an

CC antisense oligonucleotide targeted to human c-raf kinase
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGGAAG 1524
 Db 19 AGGAGGAGAGCCAGCAG 2
 RESULT 130
 ACD42099/c
 ID ACD42099 standard; DNA; 20 BP.
 XX
 AC ACD42099;
 XX
 DT 05-SEP-2003 (first entry)
 XX
 DE Antisense oligonucleotide targeting human c-raf, ISIS7853.
 XX
 KW Human; ss; antisense; c-raf; a-raf; b-raf; protein kinase; cancer;
 KW signal transduction; cell proliferation; lung carcinoma; cytostatic;
 KW antisense gene therapy; chemotherapeutic agent; angiogenesis;
 KW hyperproliferative condition; neovascularisation; ocular angiogenesis.
 XX
 OS Homo sapiens.
 OS
 PN US2003032607-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 25-JAN-2002; 2002US-00057550.
 XX
 PR 31-MAY-1994; 94US-00250856.
 PR 31-MAY-1995; 95WO-US007111.
 PR 26-NOV-1996; 96US-00756806.
 PR 07-JUL-1997; 97US-00888982.
 PR 06-JUL-1998; 98WO-US013961.
 PR 28-AUG-1998; 98US-00143214.
 PR 18-FEB-2000; 2000US-00506073.
 XX
 PA (MONI/) MONIA B P.
 XX
 PI Monia BP;
 XX
 DR WPI; 2003-503332/47.
 XX
 PT Novel antisense oligonucleotide which is targeted to mRNA encoding human
 PT raf and which is capable of inhibiting raf expression, useful for
 PT treating or preventing hyperproliferative conditions such as cancer;
 XX
 PS Disclosure; Page 8; 42pp; English.
 XX
 CC The invention relates to an oligonucleotide 8-50 nucleotides in length
 CC which is targeted to mRNA encoding human c-raf, a-raf or b-raf (raf is a
 CC protein kinase playing a regulatory role in signal transduction,
 CC regulating cell proliferation and has been implicated in lung carcinoma),
 CC and which is capable of inhibiting raf expression. Also included is a
 CC composition comprising the oligonucleotide and a pharmaceutically
 CC acceptable carrier. The antisense oligonucleotide is useful for
 CC inhibiting the expression of human raf in human cells or tissues, by
 CC contacting the human cells or tissues with the oligo. The oligo. is also
 CC useful for treating or preventing a disease or condition associated
 CC with the expression of raf by administering it in combination with a
 CC chemotherapeutic agent to a human or cells of the human, where the
 CC expression of raf is abnormal expression, and the condition is a
 CC hyperproliferative condition such as cancer, angiogenesis or
 CC neovascularisation (preferably ocular angiogenesis or
 CC neovascularisation). The oligo. is also useful for inhibiting
 CC hyperproliferation of cells. The oligos. are also useful as tools, for

CC example for detecting and determining the role of raf expression in
 CC various cell functions and physiological processes and conditions and for
 CC diagnosing conditions associated with raf expression and for research
 CC purposes. The present sequence is an antisense oligonucleotide targeting
 CC a human raf mRNA
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGAG 2
 RESULT 131
 ACA61359/C
 ID ACA61359 standard; DNA; 20 BP.
 AC ACA61359;
 XX
 DT 11-AUG-2003 (first entry)
 XX Human c-raf mRNA antisense oligonucleotide #7.
 DE Human; c-raf; antisense; ss; nuclease inhibitor; gene therapy; AIDS;
 KW bacterial infection; viral infection; protozoan infection;
 KW abnormal cell proliferation; tumour formation; atherosclerosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 Key Location/Qualifiers
 modified_base 1..20
 /tag= a
 /mod_base= OTHER
 /note= "OTHER = phosphorothioate backbone. Optionally 10-
 20 are 2'-O-methyl nucleotides"
 XX
 US2003004325-A1.
 XX
 PD 02-JAN-2003.
 XX
 PF 28-NOV-2001; 2001US-00996263.
 XX
 PR 11-JAN-1990; 90US-00463358.
 PR 13-AUG-1990; 90US-00566977.
 PR 11-JAN-1991; 91WO-US000243.
 PR 12-AUG-1991; 91WO-US005720.
 PR 24-DEC-1991; 91US-00814961.
 PR 05-MAR-1992; 92US-00835932.
 PR 01-JUL-1992; 92US-0084634.
 PR 23-DEC-1992; 92WO-US011339.
 PR 21-JUN-1994; 94US-00244993.
 PR 06-JUN-1995; 95US-00471973.
 PR 17-AUG-1998; 98US-00135202.
 XX
 (ISIS-) ISIS PHARM INC.
 XX
 Cook PD, Kawasaki AM;
 WPI; 2003-438873/41.
 XX
 New nuclease resistant compounds, useful as therapeutics, diagnostic
 PT agents, or research reagents, or for treating an organism with a disease
 PT associated with the undesired production of a protein, e.g. bacterial
 PT infections or AIDS.
 XX
 Example 31; Page 29; 50pp; English.
 PS
 XX The invention relates to a nuclease resistant compound that hybridises

CC with RNA or DNA, comprising covalently-bound nucleosides that
 CC individually include a ribose or deoxyribose sugar portion and a base
 CC portion. The nuclease resistant compounds are useful as therapeutics,
 CC diagnostic agents, or research reagents. The compounds are also useful
 CC for modulating the activity of an RNA or DNA molecule, or for treating an
 CC organism with a disease associated with the undesired production of a
 CC protein, e.g. bacterial, viral or protozoan infections, AIDS, abnormal
 CC cell proliferation and tumour formation, or atherosclerosis. The present
 CC sequence represents the human c-raf mRNA antisense oligonucleotide #7
 XX
 SQ Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1507 AGGAGGAGAGCCAGAG 1524
 Db 19 AGGAGGAGAGCCAGAG 2
 RESULT 132
 ADD44696/C
 ID ADD44696 standard; DNA; 20 BP.
 XX
 AC ADD44696;
 XX
 DT 15-JAN-2004 (first entry)
 XX Human c-Raf antisense oligonucleotide #7.
 DE Human; ss; antisense; C-Raf; virucide; anti-HIV; antiarteriosclerotic;
 KW cytostatic; 2'-fluoro substituent; AIDS; atherosclerosis; cancer.
 XX
 OS Homo sapiens.
 XX
 FN US2003187240-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 28-JAN-2003; 2003US-00352586.
 XX
 PR 11-JAN-1990; 90US-00463358.
 PR 13-AUG-1990; 90US-00566977.
 PR 05-MAR-1992; 92US-00835932.
 PR 06-JUN-1995; 95US-00468037.
 PR 02-SEP-1999; 99US-00389283.
 XX
 (ISIS-) ISIS PHARM INC.
 XX
 Cook PD, Kawasaki AM;
 WPI; 2003-831271/77.
 XX
 Modified oligonucleotides useful as therapeutics, diagnostics and
 PT research agents comprises several covalently bound nucleosides joined by
 PT internucleoside linkages.
 XX
 Example 31; SEQ ID NO 13; 48pp; English.
 XX
 The invention relates to a modified oligonucleotide comprising several
 CC covalently bound nucleosides including a ribose or deoxyribose sugar
 CC portion and a base portion. The nucleosides are joined together by
 CC internucleoside linkages such that the base portion of the nucleosides
 CC form a mixed base sequence. At least one of the nucleosides includes a
 CC modified ribofuranosyl moiety bearing a 2'-fluoro substituent. The
 CC antisense oligonucleotides of the invention are useful as therapeutics,
 CC diagnostics and research agents e.g. for the treatment of various viruses
 CC (e.g. AIDS), for modulating the production of proteins by an organism,
 CC treating an organism having a disease involving an undesired production
 CC of a protein (e.g. atherosclerosis, cancer), detecting the presence or
 CC absence of abnormal RNA molecules, or abnormal or inappropriate
 CC expression of normal RNA molecules in organisms or cells, and for the

CC selective binding of RNA for use as research reagents and diagnostic
 CC agents. The compounds have improved stability to enzymatic degradation
 CC with various intracellular and extracellular nucleases, and improved
 CC ability to bind to a specific DNA or RNA with fidelity compared to wild-
 CC type DNA-DNA and RNA-DNA duplexes and phosphorus-modified oligonucleotide
 CC duplexes containing methylphosphonates, phosphoramidates and phosphate
 CC triesters. The present sequence is an antisense oligonucleotide of the
 CC invention targeting human c-Raf.

XX Sequence 20 BP; 0 A; 10 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 76;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGGAGGAGGAGG 1524
 DB 19 AGGAGGAGGAGGAGGAGG 2

RESULT 133

AAF03299/C
 ID AAF03299 standard; DNA; 17 BP.

AC AAF03299;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #1594.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

OS Homo sapiens.

PN WO2000061729-A2.

PD 19-OCT-2000.

PF 11-APR-2000; 2000WO-US009721.

PR 12-APR-1999; 99US-0129390P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Zwick M, Pavco P, Mcswiggen J;

DR WPI; 2000-647423/62.

PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.

PS Claim 37; Page 92; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha

XX Sequence 17 BP; 3 A; 1 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 76;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1415 CAACTTCAAAAGGCA 1431
 DB 17 CAACTTCAAAAGGCA 1

RESULT 134

AAF03298/C

ID AAF03298 standard; DNA; 17 BP.

XX AAF03298;

DT 16-FEB-2001 (first entry)

DE Hammerhead ribozyme substrate #1593.

XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.

OS Homo sapiens.

PN WO2000061729-A2.

PD 19-OCT-2000.

PF 11-APR-2000; 2000WO-US009721.

PR 12-APR-1999; 99US-0129390P.

PA (RIBO-) RIBOZYME PHARM INC.

PI Blatt L, Zwick M, Pavco P, Mcswiggen J;

DR WPI; 2000-647423/62.

PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.

PS Claim 37; Page 92; 164pp; English.

CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha

XX Sequence 17 BP; 3 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 76;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1417 ACTTCAAAAGGCAAG 1433

DB 17 ACTTCAAAAGGCAAG 1

RESULT 135

AAA10583/C

ID AAA10583 standard; DNA; 18 BP.

XX AAA10583;

DT 29-JUN-2000 (first entry)

DE Smad2 antisense oligonucleotide sequence #36 (ISIS# 27813).

XX Smad2; MADH2; MADR2; hMAD2; JVI8-1; transcription factor; inflammation;
 KW chromosome 18q21; antisense compound; treat; prevent; infection; tumour;
 KW diagnostic reagent; research reagent; ss; cancer.

OS Synthetic.

PN US6037142-A.
 PD 14-MAR-2000.
 XX 23-FEB-1999; 99US-00255912.
 XX 23-FEB-1999; 99US-00255912.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Cowser LM;
 PI WPI; 2000-269886/23.
 DR New antisense compound that inhibits human Smad2, useful e.g. for
 PT treating or preventing infection, inflammation and tumors.
 XX Claim 11; Col 39; 31pp; English.
 XX This sequence represents an antisense nucleotide sequence targeting human
 CC Smad2. Smad2 is also known as MADH2, MADR2, hMAD2 and JVI18-1, and is a
 CC member of a subgroup of Smad family transcription factors which are
 CC cytosolic proteins regulated by transforming growth factor-beta (TGF-
 CC beta) and activins. Smads exist as monomers in unstimulated cells as homo
 CC - or heterodimerise and translocate to the nucleus and activate target
 CC gene transcription upon ligand binding. The Smad2 gene is located on
 CC chromosome 18q21. The invention relates to antisense compounds (see
 CC AAA10548-A10587) targeted to the Smad2 nucleotide sequence. The antisense
 CC oligonucleotide sequences inhibit Smad2 expression by hybridising to DNA
 CC or RNA. The antisense nucleotides are used to treat or prevent diseases
 CC associated with expression of Smad2, e.g. infection, inflammation and
 CC tumours. The oligonucleotides can also be used as diagnostic or research
 CC reagents
 XX
 SQ Sequence 18 BP; 5 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 84;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1557 TGAATGACCTCTCCAG 1573
 DB 18 TGAATGACCTCTACAG 2
 RESULT 136
 AAZ70696/c
 XX AAZ70696 standard; DNA; 18 BP.
 XX AAZ70696;
 XX 10-SEP-2001 (first entry)
 XX Human biallelic marker upstream amplification primer SEQ ID NO:5052.
 XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 XX WO9954500-A2.
 XX 28-OCT-1999.
 XX 21-APR-1999; 99WO-IB0000822.
 XX 21-APR-1998; 98US-0082614P.
 XX 23-NOV-1998; 98US-0109732P.
 XX (GIST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX Claim 8; Page 1308; 2745pp; English.
 XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 18 BP; 1 A; 8 C; 0 G; 9 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 84;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1469 AGAGGAGAGGAGGAA 1485
 DB 17 AGAGGAGAGGAGGAA 1
 RESULT 137
 AAZ53136
 ID AAZ53136 standard; DNA; 15 BP.
 XX AAZ53136;
 XX 30-MAR-2001 (first entry)
 XX IGF-I oligonucleotide #4096.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 87; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4511 and AAF4513-F4516). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1395 GGGGGCGCGAAGAAC 1409
DB 1 GGGGGCGCGAAGAAC 15

RESULT 138
AAAX22495/C
ID AAX22495 standard; RNA; 18 BP.
XX AC AAX22495;
XX DT 25-MAR-2003 (revised)
XX DT 21-MAY-1999 (first entry)
XX DE Streptomyces sp. est gene RBS RNA fragment.
XX KW Xylanase; acidophilic; thermostable; XYL I; XYL II; plant biomass;
XX KW hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
XX KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin; ds.
XX OS Streptomyces sp.
XX PN US5871730-A.
XX PD 16-FEB-1999.
XX PF 29-JUL-1994; 94US-00282197.
XX PR 29-JUL-1994; 94US-00282197.
XX FA (UYSH) UNIV SHERBROOKS.
XX PI Beaulieu C, Brzezinski R, Dery CV;
XX DR WPI; 1996-141348/14.
XX PT New acidophilic and thermostable xylanase enzymes from Actinomadura sp.
XX PT FC7 - useful for treating plant biomass, especially paper and wood pulp,
XX PT to degrade hemicellulose and hydrolyse xylan.
XX PS Example 7; Fig 7; 60pp; English.
XX CC This invention describes the use of novel acidophilic and thermostable xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which retain their activity under harsh industrial conditions (e.g. high

temperature or wide pH ranges) and may be secreted by recombinant host cells, to treat plant biomass. Xylanases XYL I and XYL II are part of a large group of hemicellulase enzymes and function by cutting the beta-1,4 bonds within the xylosic chain of xylan (a polymer of D-xylose residues that is a major constituent of hemicellulose). This means that they may be used in the paper and pulp industry to improve the efficiency of the bleaching process by degrading the structure of the material. XYL I and XYL II may also be used to treat feed, by degrading a substrate with a high beta-glucan or cellulose content. XYL I and XYL II retain their activity at high temperatures (e.g. 70 deg. C) and at low pHs (e.g. 4.0), conditions which tend to denature most known xylanases. Enzymes that remain active in these conditions may be used in industrial processes that are carried out at high temperature and low pH to speed up other, non-enzymatic reactions, minimising costs, energy requirements, and the risk of pollution, (e.g. enzymes XYL I and XYL II can be used to facilitate chlorine bleaching of paper pulp which is carried out in hot, acidic conditions). Pretreatment with XYL I and XYL II, allows the bleaching agents to penetrate better, to remove lignin from the pulp and 'bleach' the colouration from it. This means smaller quantities of the agents can be used to produce the same or a better result. Also, disrupting the structure aids water drainage. NOTE: This patent is an equivalent to FI9503640. (Updated on 25-MAR-2003 to correct DR field.)

Sequence 18 BP; 6 A; 4 C; 6 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 689 CATGACTGTGCTTTTCA 706
DB 18 CATGCTGTGCCCTTCA 1

RESULT 139
AAV00348/C
ID AAV00348 standard; DNA; 18 BP.
XX AC AAV00348;
XX DT 23-APR-1998 (first entry)
XX DE Insecticidal gene sequence modification oligonucleotide BTK53.
XX KW Insecticidal protein; Bacillus thuringiensis; monocotyledonous plant;
XX KW structural gene; maize; CryI(b); CryIIb; ss.
XX OS Synthetic.
XX OS Bacillus thuringiensis.
XX PN US5689052-A.
XX PD 18-NOV-1997.
XX PF 19-SEP-1995; 95US-00530492.
XX PR 22-DEC-1993; 93US-00172333.
XX PA (MONS) MONSANTO CO.
XX PI Sanders PR, Brown SM, Dean DA, Fromm ME;
XX DR WPI; 1998-008070/01.
XX PT Genes encoding insecticidal proteins of Bacillus thuringiensis - modified to enhance expression in monocotyledonous plants.
XX PS Example 1; Col 16; 86pp; English.
XX CC The present sequence represents an oligonucleotide used in the present invention describing new structural genes capable of being expressed in a monocotyledonous plant. The new genes comprise modified nucleotide sequences which encode insecticidal proteins of Bacillus thuringiensis.

CC The genes have been modified to reduce the usage of codons that are rare
 CC or semi-rare in monocotyledon DNA, thereby increasing transformation
 CC efficiency and/or increasing accumulation of the insecticidal protein in
 CC monocotyledon tissues
 XX
 SQ Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 646 ATGGTGACGGCGTGAAG 663
 |||||
 Db 18 ATGGTGGCGGCTCGAAG 1

RESULT 140
 AAZ94539
 ID AAZ94539 standard; DNA; 18 BP.
 XX
 AC AAZ94539;
 XX
 DT 18-JUL-2000 (first entry)
 XX
 DE Human cytokine receptor zalphall sense PCR primer ZC19954.
 XX
 KW Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;
 KW signal transduction; growth factor; cancer; tumour; infection;
 KW gene therapy; diagnosis; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200017235-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 23-SEP-1999; 99WO-US022149.
 XX
 PR 23-SEP-1998; 98US-00159254.
 PR 09-MAR-1999; 99US-00265117.
 PR 06-JUL-1999; 99US-00347930.
 XX
 PA (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
 XX WPI; 2000-292825/25.
 XX
 PT Novel nucleic acid encoding zalphall polypeptide, useful for treating
 PT e.g. viral infection or tumors, and for identifying ligands that
 PT stimulate cell proliferation.
 XX
 PS Example 3; Page 155; 190pp; English.
 XX
 CC The present sequence is that of oligonucleotide ZC19954, used as sense
 CC primer in the PCR based mapping of the human zalphall gene to the 16p11.1
 CC region of chromosome 16. Zalphall (see also AAY79312) is a novel class I
 CC cytokine receptor that may be involved in an apoptotic cellular pathway,
 CC or is a cell-cell signalling molecule, growth factor receptor, or
 CC extracellular matrix associated protein with growth factor hormone
 CC activity. The invention provides zalphall polypeptides, polynucleotides
 CC and antibodies, and methods for their use in the treatment and diagnosis
 CC of conditions associated with altered zalphall expression or activity
 XX
 SQ Sequence 18 BP; 2 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 511 ATGGGCTGGGGGCTGC 528
 |||||
 Db 1 ACTGGGCTGGGGGCTGC 18

RESULT 141
 AAF73266/C
 ID AAF73266 standard; DNA; 18 BP.
 XX
 AC AAF73266;
 XX
 DT 26-APR-2001 (first entry)
 XX
 DE Oligonucleotide #57.
 XX
 KW CryIA; transgenic; crystal; toxin; insecticide; ss.
 XX
 OS Synthetic.
 XX
 PN US6180774-B1.
 XX
 PD 30-JAN-2001.
 XX
 PF 05-AUG-1997; 97US-00906517.
 XX
 PR 22-DEC-1993; 93US-00172333.
 PR 19-SEP-1995; 95US-00530492.
 XX
 PA (MONS) MONSANTO CO.
 XX
 KW Brown SM, Dean DA, Fromm ME, Sanders PR;
 WPI; 2001-190861/19.
 XX
 PT Novel nucleic acids, useful for transgenic plant production which is
 PT capable of expressing increased levels of desired proteins.
 XX
 PS Example 1; Col 16; 81pp; English.

XX The present invention relates to nucleotides 669-1348 of a
 CC B.thuringiensis CryIA(b). The invention is useful for transgenic plant
 CC production, e.g. maize, capable of expressing increased amount of
 CC transgenic protein, e.g. crystal protein toxin gene of Bacillus
 CC thuringiensis
 XX
 SQ Sequence 18 BP; 3 A; 9 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 646 ATGGTGACGGCGTGAAG 663
 |||||
 Db 18 ATGGTGGCGGCTCGAAG 1

RESULT 142
 AAS20658
 ID AAS20658 standard; DNA; 18 BP.
 XX
 AC AAS20658;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human zalphall receptor sequencing primer ZC19954.
 XX
 KW Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
 KW natural killer cell proliferation; T-cell proliferation;
 KW B-cell proliferation; anti-tumour response; immune system;
 KW immunostimulant; cytostatic; human; sequencing primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6307024-B1.
 XX
 PD 23-OCT-2001.

```

XX 09-MAR-1999; 2000US-00522217.
XX 09-MAR-1999; 99US-0123547P.
XX 11-MAR-1999; 99US-0123904P.
XX 01-JUL-1999; 99US-0142013P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnson JV, Nelson AU, Dillon SR, Hammond AK;
XX WPI; 2002-040208/05.
XX New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX Example 3; Col 133; 105pp; English.
XX The present invention relates to the isolation of a novel cytokine,
CC zalphall Ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
CC zalphall Ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall Ligand gene,
CC and in gene therapy. Zalphall Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a sequencing primer used to sequence DNA encoding human zalphall receptor
CC in the methods of the present invention.
XX Sequence 18 BP; 2 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTGGGCTGGGGCTGTC 528
DB 1 ACTGGGCTGGGGACTGC 18
RESULT 143
AAD61901
ID AAD61901 standard; DNA; 18 BP.
XX AAD61901;
AC AAD61901;
XX 15-JAN-2004 (first entry)
XX Human Zalphall DNA mapping PCR primer, ZC19,954.
XX Cytokine receptor; Zalphall; cell proliferation; cell development;
KW splenic disorder; blood disorder; bone disorder; immune disorder;
KW haematopoietic; lymphoid; inflammatory; therapy; human; PCR; primer; ss.
XX Homo sapiens.
XX US6576744-B1.
XX 10-JUN-2003.
XX 23-SEP-1999; 99US-00404641.
XX 23-SEP-1998; 98US-0100896P.
XX 09-MAR-1999; 99US-0123546P.
XX 06-JUL-1999; 99US-0142574P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
PI WPI; 2003-799829/75.
XX Novel cytokine receptor Zalphall useful for treating lymphoid, immune,
PT inflammatory, splenic, blood or bone disorders.
XX Example 3; Col 89; Opp; English.
XX The invention relates to a cytokine receptor designated Zalphall and its
CC nucleic acid sequence. Zalphall protein is useful for detecting ligands
CC that stimulate the proliferation and/or development of haematopoietic,
CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
CC in identifying a region of the genome associated with human disease
CC states. Zalphall protein is useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. The present sequence is
CC a PCR primer used for mapping human Zalphall DNA
XX Sequence 18 BP; 2 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTGGGCTGGGGCTGTC 528
DB 1 ACTGGGCTGGGGACTGC 18
RESULT 144
AAD61918
ID AAD61918 standard; DNA; 18 BP.
XX AAD61918;
AC AAD61918;
XX 15-JAN-2004 (first entry)
XX Human MPL-Zalphall chimera specific primer, ZC19,954.
XX Cytokine receptor; Zalphall; cell proliferation; cell development;
KW splenic disorder; blood disorder; bone disorder; immune disorder;
KW haematopoietic; lymphoid; inflammatory; therapy; MPL receptor; human;
KW primer; ss.
XX Homo sapiens.
XX US6576744-B1.
XX 10-JUN-2003.
XX 23-SEP-1999; 99US-00404641.
XX 23-SEP-1998; 98US-0100896P.
XX 09-MAR-1999; 99US-0123546P.
XX 06-JUL-1999; 99US-0142574P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
PI WPI; 2003-799829/75.
XX Novel cytokine receptor Zalphall useful for treating lymphoid, immune,
PT inflammatory, splenic, blood or bone disorders.
XX Example 6; Col 95; Opp; English.
XX The invention relates to a cytokine receptor designated Zalphall and its

```

```

PR 09-MAR-1999; 99US-0123546P.
PR 06-JUL-1999; 99US-0142574P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX WPI; 2003-799829/75.
XX Novel cytokine receptor Zalphall useful for treating lymphoid, immune,
PT inflammatory, splenic, blood or bone disorders.
XX Example 3; Col 89; Opp; English.
XX The invention relates to a cytokine receptor designated Zalphall and its
CC nucleic acid sequence. Zalphall protein is useful for detecting ligands
CC that stimulate the proliferation and/or development of haematopoietic,
CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
CC in identifying a region of the genome associated with human disease
CC states. Zalphall protein is useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. The present sequence is
CC a PCR primer used for mapping human Zalphall DNA
XX Sequence 18 BP; 2 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTGGGCTGGGGCTGTC 528
DB 1 ACTGGGCTGGGGACTGC 18
RESULT 144
AAD61918
ID AAD61918 standard; DNA; 18 BP.
XX AAD61918;
AC AAD61918;
XX 15-JAN-2004 (first entry)
XX Human MPL-Zalphall chimera specific primer, ZC19,954.
XX Cytokine receptor; Zalphall; cell proliferation; cell development;
KW splenic disorder; blood disorder; bone disorder; immune disorder;
KW haematopoietic; lymphoid; inflammatory; therapy; MPL receptor; human;
KW primer; ss.
XX Homo sapiens.
XX US6576744-B1.
XX 10-JUN-2003.
XX 23-SEP-1999; 99US-00404641.
XX 23-SEP-1998; 98US-0100896P.
XX 09-MAR-1999; 99US-0123546P.
XX 06-JUL-1999; 99US-0142574P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
PI WPI; 2003-799829/75.
XX Novel cytokine receptor Zalphall useful for treating lymphoid, immune,
PT inflammatory, splenic, blood or bone disorders.
XX Example 6; Col 95; Opp; English.
XX The invention relates to a cytokine receptor designated Zalphall and its

```

CC nucleic acid sequence. Zalphall protein is useful for detecting ligands
 CC that stimulate the proliferation and/or development of haematopoietic,
 CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
 CC in identifying a region of the genome associated with human disease
 CC states. Zalphall protein is useful for treating lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. The present sequence is
 CC a primer used for sequence analysis of human MPL-Zalphall chimera. This
 CC sequence is used in the exemplification of the invention

SQ Sequence 18 BP; 2 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 511 ATTGGGCTGGGGGCTGC 528
 Db 1 ACTGGGCTGGGGGACTGC 18
 |||||

RESULT 145

AAC72366
 ID AAC72366 standard; DNA; 17 BP.

XX AC AAC72366;

DT 09-FEB-2001 (first entry)

XX Single nucleotide polymorphism PCR primer #1464.

XX Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; PCR primer; ss.

XX Homo sapiens.

XX WO200058519-A2.

XX 05-OCT-2000.

XX 30-MAR-2000; 2000WO-US008440.

XX 31-MAR-1999; 99US-0127248P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.

XX Althuler D, Cargill M, Daley GO, Ireland JS, Lander ES;
 PI Lipshutz RJ, Patil N, Sklar P;

XX WPI; 2000-611722/58.

XX Nucleic acid selected from one of 106 genes comprising single nucleotide
 PT polymorphisms, allele-specific oligonucleotides to the genes are useful
 PT for phenotypic correlations, forensics, paternity testing, medicine and
 PT genetic analysis.

PS Claim 8; Fig 5; 214pp; English.

XX The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases

SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1237 CACCTGGGTCACAAAC 1252
 Db 1 CAGCTGGGTCACAAAC 16
 |||||

RESULT 146

AAC72375
 ID AAC72375 standard; DNA; 17 BP.

XX AC AAC72375;

DT 09-FEB-2001 (first entry)

XX Single nucleotide polymorphism PCR primer #1470.

XX Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; PCR primer; ss.

XX Homo sapiens.

XX WO200058519-A2.

XX 05-OCT-2000.

XX 30-MAR-2000; 2000WO-US008440.

XX 31-MAR-1999; 99US-0127248P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFFY-) AFFYMETRIX INC.

XX Althuler D, Cargill M, Daley GO, Ireland JS, Lander ES;
 PI Lipshutz RJ, Patil N, Sklar P;

XX WPI; 2000-611722/58.

XX Nucleic acid selected from one of 106 genes comprising single nucleotide
 PT polymorphisms, allele-specific oligonucleotides to the genes are useful
 PT for phenotypic correlations, forensics, paternity testing, medicine and
 PT genetic analysis.

PS Claim 9; Fig 5; 214pp; English.

XX The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases

SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1237 CACCTGGGTCACAAAC 1252
 Db 1 CAGCTGGGTCACAAAC 16
 |||||

RESULT 147

AAF03297/C
 ID AAF03297 standard; DNA; 17 BP.

XX AC AAF03297;

Blatt L, Zwick M, Pavco P, Mcswiggen J;
WPI; 2000-647423/62.
Enzymatic and antisense nucleic acid inhibition of repressor genes,
useful for producing e.g. granulocyte colony stimulating factor protein,
interferon alpha and erythropoietin.
Claim 37; Page 92; 16app; English.

The present invention relates to enzymatic and antisense nucleic acid
molecules that act as inhibitors of the expression of repressor genes
encoding the TR2 Orphan receptor, EAR3/CODP-Tr-1, the GATA transcription
factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
Inhibition of the repressors removes prevents inhibition (and
consequently increases expression of) genes involved in the production of
erythropoietin, granulocyte colony stimulating factor protein and
interferon alpha

Sequence 17 BP; 4 A; 1 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred.No.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1415 CAACTTCAAAAGGCC 1430
|||||
Db 16 CAACTTCAAAAGGCC 1

RESULT 149
ABK03667/C

ID ABK03667 standard; RNA; 17 BP.

XX AC ABK03667;
XX AC ABK03667;
XX DT DT
XX DE DE
XX DE Human CD20 Amberyze #16.
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
DNazyme; incyzyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
MCL; immunocyctoma; IMC; immune thrombocytopaenia; stroke; dementia;
inflammatory arthropathy; central nervous system injury;
cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
Parkinson's disease; ataxia; Huntington's disease;
Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.
OS Synthetic.
XX WO200159103-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-US004273;
XX PR 11-FEB-2000; 2000US-0181797P.
XX PR 28-FEB-2000; 2000US-0185516P.
XX PR 06-MAR-2000; 2000US-0187128P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (CHOW/) CHOWIRRA B M.
XX PI Blatt L, Mcswiggen J, Chowirra BM;

16-FEB-2001 (first entry)	
Hammerhead ribozyme substrate #1592.	
Ribozyme: erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.	
Homo sapiens.	
WO200061729-A2.	
19-OCT-2000.	
11-APR-2000; 2000WO-US009721.	
12-APR-1999; 99US-0129390P.	
(RIBO-) RIBOZYME PHARM INC.	
Blatt L, Zwick M, Pavco P, Mcswiggen J;	
WPI; 2000-647423/62.	
Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.	
Claim 37; Page 92; 164pp; English.	
The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRR-2 and/or the CAAT Displacement protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha	
Sequence 17 BP; 3 A; 3 C; 4 G; 7 T; 0 U; 0 Other;	
Query Match 0.9%; Score 14.4; DB 1; Length 17;	
Best Local Similarity 93.8%; Pred. No.1e+02;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
1418 CTTCAAAAAGCCAG 1433	
17 CTTCAATATAGCCAG 2	
RESULT 148	
AAF03300/c	
ID AAF03300 standard; DNA; 17 BP.	
AC AAF03300;	
16-FEB-2001 (first entry)	
Hammerhead ribozyme substrate #1595.	
Ribozyme: erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.	
Homo sapiens.	
WO200061729-A2.	
19-OCT-2000.	
11-APR-2000; 2000WO-US009721.	
12-APR-1999; 99US-0129390P.	
(RIBO-) RIBOZYME PHARM INC.	

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX Claim 30; Page 166; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or

CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is an amberzyme molecule of the invention

XX SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1119 TTGGACACAGATTTC A 1134

Db 16 TTGGACACAGATTGCA 1

RESULT 150

ABK03088/C

XX ID ABK03088 standard; RNA; 17 BP.

XX AC ABK03088;

XX DT 12-MAR-2002 (first entry)

XX DE Human CD20 Inozyme #39.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

XX cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

XX muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

XX DNzyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;

XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

XX MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

XX inflammatory arthropathy; central nervous system injury;

XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX PD 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWIRA B M.

XX Blatt L, Mcswiggen J, Chowira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX Claim 30; Page 146; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or

CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is an inozyme of the invention

XX SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1119 TTGGACACAGATTTC A 1134

Db 17 TTGGACACAGATTGCA 2

CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e-02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 512 TTGGGCTGGGGGCTG 527
Db 17 TTGGGCTGGGGGCTG 2
RESULT 152
ABN00980/c
ID ABN00980 standard; DNA; 17 BP.
XX
AC ABN00980;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:972.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 972; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
CC -1 proteins, as standards in assays used to determine the concentration
CC

RESULT 151
ABN00979/c
ID ABN00979 standard; DNA; 17 BP.
XX
AC ABN00979;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:971.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 971; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TTGGGCTGGGGGCTG 527
|||||
Db 16 TTGGGCTGGGGGCTG 1

RESULT 153
ABQ64004/C
ID ABQ64004 standard; DNA; 17 BP.

XX AC ABQ64004;

XX DT 20-AUG-2002 (first entry)

XX DE Human KTOM1a portion (ABQ63232) probe # 717.

XX KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

XX OS Homo sapiens.

XX PN WO200224750-A2.

XX PD 28-MAR-2002.

XX PF 21-SEP-2001; 2001WO-US029656.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 28-AUG-2001; 2001US-0315676P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhang J;

XX DR WPI; 2002-479509/51.

XX PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.

PS Example 2; Page 251; 418pp; English.

XX The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumour overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (ABQ63232)

XX SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1247 CCAACGCGAGCGGATT 1262
|||||
Db 16 CCAACGCGAGCGGATT 1

RESULT 154

ABQ64003/C

ID ABQ64003 standard; DNA; 17 BP.

XX AC ABQ64003;

XX DT 20-AUG-2002 (first entry)

XX DE Human KTOM1a portion (ABQ63232) probe # 716.

XX KW Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.

XX OS Homo sapiens.

XX PN WO200224750-A2.

XX PD 28-MAR-2002.

XX PF 21-SEP-2001; 2001WO-US029656.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 28-AUG-2001; 2001US-0315676P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhang J;

XX DR WPI; 2002-479509/51.

XX PT New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.

XX Example 2; Page 251; 418pp; English.

PS The invention relates to a novel isolated nucleic acid encoding human

CC KTM01 (kidney tumour overexpressed membrane) protein. The protein of the

CC invention has cytostatic activity. The nucleotide may have a use in gene

CC therapy. The KTM01 nucleic acids may be used to diagnose, treat or

CC monitor a disease caused by altered expression of human KTM01.

CC Compositions comprising the nucleic acids, proteins or antibodies may be

CC used to treat subjects having defects in KTM01 which can manifest as

CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,

CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta

CC function. The sequence represents a probe used in the invention to scan

CC the nt 1-1001 portion of human KTM01a (ABQ63232)

XX

SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1247 CCACACGCGAGCGGATT 1262

DB 17 CCACATGCGCGGATT 2

RESULT 155

AAQ11746

ID AAQ11746 standard; DNA; 18 BP.

XX

AC AAQ11746;

XX

DT 24-OCT-2003 (revised)

DT 27-AUG-2003 (revised)

DT 02-AUG-1991 (first entry)

XX

DE Target duplex from Herpes Simplex genome.

XX

XX Triple helix; anti-sense therapy; switchback; polarity reversal; ds.

XX

OS Viruses.

XX

PN WO9106626-A.

XX

PD 16-MAY-1991.

XX

PF 23-OCT-1989; 89US-00425803.

XX

PR 23-OCT-1989; 89US-00425803.

PR 29-MAR-1990; 90US-00502272.

PR 30-JUL-1990; 90US-00559958.

XX

PA (GILE-) GILEAD SCI INC.

XX

XX Froehner B, Toole JU;

XX

XX WPI; 1991-164176/22.

XX

PT Oligo;nucleotide triple helix with double-helical nucleotide duplex -

PT useful in anti-sense therapy, to inhibit e.g. viral polymerase(s), or

PT interfere with binding factors to nucleic acids.

XX

PS Disclosure; Fig 4A; 61pp; English.

XX

XX The sequence is a target for novel oligonucleotides which comprise a 1st

CC sequence (S1) of at least 3 bases with 3'-5' or 5'-3' polarity,

CC coupled to a 2nd sequence (S2) of at least one base having the opposite

CC polarity. S1 and S2 are joined by 5'-5'; 3'-3'; base-5'; 5'-base; base-3,

CC ; or 3'-base linkages opt. through a linker. Other oligonucleotides

CC comprise a sequence (S3) of at least 3 bases enriched in purine

CC residues, and a sequence (S4) of at least 3 bases enriched in

CC pyrimidines. Both types of oligos react with strands of target duplex DNA

CC to form a triplex. They are therefore useful in antisense therapy to

CC inactivate undesirable DNA or RNA and can also inhibit viral polymerases,

CC interfere with nucleic acid binding factors, induce interferon prodn.

CC etc. Oligos with a polarity reversal have better stability against

CC nuclease degradation. An oligo specific for the Herpes target duplex was

CC designed to have the formula: 5'-TTTTTTTTTTT-3'-linker-3'-CCCC-5'.

CC It contains a region of inverted polarity but maintains the CT motif

CC throughout. It effects a crossover between the upper strand in which T

CC residues target the A-rich portion of the inverted polarity of the polyC

CC tract which targets the polyG region in the opposite strand. (Updated on

CC 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to standardise

CC OS field)

XX

SQ Sequence 18 BP; 12 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1453 AAAAGAGAAAGACCC 1468

DB 2 AAAAGAGAAAGACCC 17

RESULT 156

AAQ68779/c

ID AAQ68779 standard; DNA; 18 BP.

XX

AC AAQ68779;

XX

DT 19-FEB-1995 (first entry)

XX

DE CHA255 light chain CDR3 wild type coding sequence.

XX

XX Polymerase chain reaction; primer; PCR; amplify; heavy; light; chain;

XX complementarity determining region; CDR; variable; constant; region;

XX monoclonal antibody; MAb; binding affinity; EDTA; DOTA; tumour; cancer;

XX colorectal; breast; metal chelate; hapten; ss.

XX

OS Synthetic.

XX

PN AU9350602-A.

XX

PD 26-MAY-1994.

XX

PF 10-NOV-1993; 93AU-00050602.

XX

PR 12-NOV-1992; 92US-00975230.

XX

PA (HYBR-) HYBRITECH INC.

XX

XX Ahrweiler PM, Moore MD;

XX

XX WPI; 1994-209063/26.

XX

XX P-PSDB; AAR54177.

XX

PT Polypeptide used in imaging and treatment of carcinomas and tumours -

PT comprising substd antibody CDR having binding affinity for metal chelate

PT of EDTA or DETA or analogues.

XX

XX Claim 25; Fig 3B; 61pp; English.

XX

XX The sequences given in AAQ68779-88 encode the wild type and mutagenised

CC versions of the complementarity determining region 3 (CDR3) of the

CC antibody designated CHA255 light chain. CHA255 is a murine monoclonal

CC antibody (Mab) which is capable of binding complexes. Mutagenesis of

CC these CDRs, causes the production of polypeptides with a particularly

CC high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3 of

CC the heavy chain, and CDR2 and -3 of the light chain were targeted for

CC mutagenesis. Five residues of both CDR1 and -3 of the CHA255 heavy chain,

CC five of seven residues of light chain CDR and six of nine light chain

CC CDR3 residues were specifically targeted for codon-based mutagenesis. The

CC mutagenised Mab's can be used in compositions for in vivo imaging of

CC malignant tissues or tumours. They are also useful for the treatment of

CC malignant tissues or tumours eg. colorectal or breast cancer. Both
CC methods involve the use of radionuclides which bind to metal chelates or
CC haptens which are specifically delivered to the target site by a
CC targeting molecule. CDR derived peptides may be used to construct bi-
CC functional antibodies having dual specificities, or as donor or
CC recipients of CDR sequences

XX
SQ Sequence 18 BP; 4 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 611 CCAGAGGCTGCTAC 626
Db 18 CCAGAGTTCGTAC 3

RESULT 157
AAV57517/C
ID AAV57517 standard; DNA; 18 BP.
XX
AC AAV57517;
XX
XX 20-NOV-1998 (first entry)
XX
XX Zcytor7 cytokine receptor encoding cDNA amplifying outer nest primer.
XX
XX Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;
KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;
KW agonist; cell proliferation; cell differentiation; renal disease; human;
KW neural disease; pancreatic disease; PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9837193-A1.
XX
XX 27-AUG-1998.
XX
XX 18-FEB-1998; 98WO-US03029.
XX
XX 20-FEB-1997; 97US-00803305.
PR 02-OCT-1997; 97US-00943087.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Lok S, Kho CJ, Jeimberg AC, Adams RL, Whitmore TE, Farrah TM;
XX WPI; 1998-480798/41.
XX
XX Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful for
PT treating renal, neural, pancreatic and prostatic diseases.
XX
XX Example 1; Page 62; 72pp; English.

XX
XX Sequences shown in AAV57517 to AAV57524 represent primers used for the
CC PCR amplification of the cDNA encoding the Zcytor7 cytokine receptor.
CC Zcytor7 is a ligand-binding receptor polypeptide and is a novel member of
CC the type 2 cytokine receptor family (CRF2). An expression vector
CC containing the Zcytor7 polynucleotide, operably linked to transcription
CC promoter, a sequence encoding a transmembrane and intracellular domain,
CC or both, and a transcriptional terminator can be used to transform host
CC cells for the recombinant production of the polypeptide. The sequences
CC can be used to study the Zcytor7 gene and to isolate ligands binding to
CC it. Zcytor7 is preferentially expressed in the kidney, pancreas, prostate
CC or nervous tissue. Agonists of Zcytor7 can be used to stimulate
CC proliferation and differentiation of cell in these organs. The
CC antagonists and agonists can also be used in the treatment of renal,
CC neural, pancreatic and prostate diseases

XX
SQ Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1455 AAAGAGAAAGCCAG 1470
Db 17 AAAGAGAAACCCAG 2

RESULT 158
AAV52697
ID AAV52697 standard; DNA; 18 BP.
XX
XX AAV52697;
XX
XX 30-JUN-1999 (first entry)
XX
XX Human genome biallelic marker primer 65.
XX
XX Biallelic marker; human; high density disequilibrium map; disease; trait;
KW identification; Alzheimer's disease; drug response; drug efficacy;
KW drug toxicity; primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9904038-A2.
XX
XX 28-JAN-1999.
XX
XX 17-JUL-1998; 98WO-IB001193.
PF
XX 18-JUL-1997; 97EP-00401740.
PR 21-APR-1998; 98US-0082614P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Tchoumakov I;
PI WPI; 1999-132278/11.
XX
XX Production of biallelic markers - by obtaining a genomic DNA library;
PT determining the order and sequence of DNA fragments and identifying
PT nucleotides which vary between individuals.
XX
XX Example 7; Page 212; 288pp; English.

XX
XX This invention describes a novel method for obtaining a set of biallelic
CC markers represented in AAV52533-X52632 and AAV52833-X52843 for use in
CC constructing a high density equilibrium map of the human genome. The
CC method involves (a) obtaining a nucleic acid library comprising genomic
CC DNA fragments comprising the full genome or a portion (b) determining the
CC order of genomic DNA fragments in the genome, (c) determining the
CC sequence of selected regions of the genomic DNA fragments and (d)
CC identifying nucleotides in the genomic DNA fragments which vary between
CC individuals, thereby defining a set of biallelic markers. The methods can
CC be used for identifying traits such as disease (e.g. Alzheimer's
CC disease), drug response, drug efficacy and drug toxicity. They can be
CC used for selecting an individual for inclusion in a clinical trial. The
CC method is used to map the position of genes in a genome (preferably the
CC human genome). The sequences described in AAV52633-X52832 and AAV52844-
CC X52868 represent primers used in the method of the invention

XX
SQ Sequence 18 BP; 9 A; 4 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1457 AGAGAAAGCCAG 1472
Db 1 AGAGAAAGCCAG 16

```

XX OS Homo sapiens.
XX ID AAA49365 standard; DNA; 18 BP.
XX AC AAA49365;
XX DT 25-SEP-2000 (first entry)
XX DE Sequencing primer for Neisseria meningitidis Hsp70 gene.
XX KW Hsp70; Hsp60; heat shock protein; immunogen; immunity; vaccine;
XX KW detection; Neisseria meningitidis; Aspergillus fumigatus;
XX KW Candida glabrata; primer; ss.
XX OS Synthetic.
XX PN WO200034465-A2.
XX PD 15-JUN-2000.
XX PF 01-DEC-1999; 99WO-CA001152.
XX PR 08-DEC-1998; 98US-00207388.
XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX PI Wisniewski J;
XX DR WPI; 2000-423415/36.
XX PT Isolated nucleic acid molecule for eliciting immune response in mammal
XX PT encodes Neisseria meningitidis heat shock protein 70, Aspergillus
XX PT fumigatus Hsp60 and Candida glabrata Hsp60 polypeptide.
XX PS Example 3; Page 51; 118pp; English.
XX CC The Hsp70 heat shock protein or fragments derived from Neisseria
XX CC meningitidis and the Hsp60 heat shock protein or fragments derived from
XX CC Aspergillus fumigatus or Candida glabrata can be used as immunogens to
XX CC give protective immunity from these microorganisms. Nucleotide sequences
XX CC encoding these proteins are useful for producing recombinant proteins for
XX CC immunizing an animal or as probes and/or primers to detect the
XX CC microorganisms in a biological sample. Two primers (AAA49360, AAA49361)
XX CC were used to clone the Hsp70 gene of Neisseria meningitidis. This primer
XX CC was then used to confirm the sequence of the cloned gene
XX SQ Sequence 18 BP; 7 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 AAGCCAAATGCTGAGGA 298
DB 2 AAGCCAAATGCGAGGA 17

RESULT 160
AAZ69746
ID AAZ69746 standard; DNA; 18 BP.
AC AAZ69746;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker upstream amplification primer SEQ ID NO:4102.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 AAGCCAAATGCTGAGGA 298
DB 2 AAGCCAAATGCGAGGA 17

RESULT 161
AAZ74823
ID AAZ74823 standard; DNA; 18 BP.
AC AAZ74823;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:9179.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX PR 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX PA (GEST ) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I;
XX DR WPI; 2000-013267/01.
XX PT Novel biallelic markers used to construct a high density disequilibrium
XX PT map of the human genome.
XX PS Claim 8; Page 1105; 2745pp; English.
XX CC AAZ65854 to AAZ69578 represent human biallelic markers from the present
XX CC invention, which contain a polymorphic base at position 24 of their
XX CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX CC primers for the biallelic markers. The biallelic markers of the invention
XX CC have a variety of uses: they can be used for high density mapping of the
XX CC human genome, and in complex association studies and haplotyping studies
XX CC which are useful in determining the genetic basis for disease states.
XX CC Compositions and methods of the invention can also be useful for the
XX CC identification of the targets for the development of pharmaceutical
XX CC agents and diagnostic methods, as well as the characterisation of the
XX CC differential efficacious responses to and side effects from
XX CC pharmaceutical agents acting on a disease as well as other treatment.
XX CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX CC 3367, are not actually given a sequence in the Sequence Listing from the
XX CC present invention
XX SQ Sequence 18 BP; 1 A; 3 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTCGGGCTCTG 16
DB 1 ATGCTCGGTCTCTG 16

RESULT 161
AAZ74823
ID AAZ74823 standard; DNA; 18 BP.
AC AAZ74823;
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:9179.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.

```

XX 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX (CBST) GENSET.
XX Cohen D, Blumenfeld M, Chumakov I;
PI WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX Claim 8; Page 2187; 2745pp; English.
XX AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods for the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. the SEQ ID NOS 2852, 2943, 2974, 3035, 3056, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
SQ Sequence 18 BP; 9 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1457 AGAGAAGACCCAGAG 1472
Dd 1 AGAGAAGACCCAGAG 16
RESULT 162
AAF53137
ID AAF53137 standard; DNA; 15 BP.
AC AAF53137;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #4097.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
OS WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX

PI Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 87; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1396 GGGGCGCGAAGAAC 1409
Dd 1 GGGGCGCGAAGAAC 14
RESULT 163
AAF53135
ID AAF53135 standard; DNA; 15 BP.
XX AAF53135;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #4095.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
OS WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
PS Example 8; Page 87; 20lpp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotide of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 92; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;
QY 1395 GGGGGCGCGCAAGAA 1408
DB 2 GGGGGCGCGCAAGAA 15
|||||
RESULT 164
ACC67627/C
ID ACC67627 standard; DNA; 17 BP.
XX
AC ACC67627;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4874.
XX
KW Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
XX WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Tellerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 600; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour

CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration.
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 3 A; 5 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 11e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;
QY 288 AATGCTGAGGAGAT 301
DB 15 AATGCTGAGGAGAT 2
|||||
RESULT 165
AAK69652
ID AAK69652 standard; RNA; 17 BP.
XX
AC AAK69652;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #947.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 75; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAK6725 to AAK7572 represent specific examples
CC of nucleic acid molecules from the present invention.
XX
SQ Sequence 17 BP; 5 A; 4 C; 2 G; 0 T; 6 U; 0 Other;


```
Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      466 CAAAGTCTGTGAAACTT 482
DB      1 CAACUCUUGAAACUU 17

RESULT 166
AAAX73006/c
ID      AAX73006 standard; RNA; 17 BP.
XX
XX
AC      AAX73006;
XX
XX      28-JUL-1999 (first entry)
XX
XX      Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #439.
XX
XX      Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX      KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX      tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX      fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
XX      foetal liver kinase 1; ss.
XX
XX      Mus sp.
XX
XX      W09715662-A2.
XX
XX      01-MAY-1997.
XX
XX      25-OCT-1996; 96WO-US017480.
XX
XX      26-OCT-1995; 95US-0005974P.
XX
XX      11-JAN-1996; 96US-00584040.
XX
XX      (RIBO-) RIBOZYME PHARM INC.
XX      (CHIR) CHIRON CORP.
XX
XX      Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX      WPI; 1997-259017/23.
XX
XX      Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX      stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX      rheumatoid arthritis, etc., in a human patient.
XX
XX      Claim 4; Page 136; 218pp; English.
XX
XX      The present invention describes nucleic acid molecules which modulate the
XX      synthesis, expression and/or stability of a mRNA encoding 1 or more
XX      receptors of vascular endothelial growth factor (VEGF). A patient
XX      (preferably human) having a condition associated with the level of the
XX      fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX      receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX      angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX      treated by administering the nucleic acid molecule or the expression
XX      vector to the patient. AAX67275 to AAX75752 represent specific examples
XX      of nucleic acid molecules from the present invention
XX
XX      Sequence 17 BP; 6 A; 6 C; 4 G; 0 T; 1 U; 0 Other;
XX
XX      Query Match      0.9%; Score 13.8; DB 1; Length 17;
XX      Best Local Similarity 88.2%; Pred. No. 1.2e+02;
XX      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      18 CCCTGTGTGCTGTGTC 34
DB      17 CTGCTGTGTGCTGTGTC 1

RESULT 167
AAX62242
Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.2e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      495 ACGGACATCGCGGTGAA 511
DB      1 AAGUACAUCCGCCUGAA 17

RESULT 168
AAAL7513/c
ID      AAAL7513 standard; RNA; 17 BP.
XX
XX      AAAL7513;
XX
XX      19-JUN-2000 (first entry)
XX
XX      Aryl hydrocarbon nuclear transport substrate sequence SEQ ID NO:739.
XX
XX      Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis;
XX      integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX
```

KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberculous sclerosis; pot-wine stain; Sturge-Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 93WO-US006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 of an mRNA encoding an angiogenic factors.
 PT
 XX Claim 53; Page 84; 305pp; English.
 PS
 XX The present invention describes enzymatic nucleic acid molecules with RNA
 cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberculous sclerosis, pot-wine stains, Sturge-Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 1 G; 0 T; 6 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1375 ATTCTGAAGAGGAGGGA 1391
 Db |||||
 17 ATTCTGAAGAGGAGGGA 1
 RESULT 169
 AA293921/c
 ID AA293921 standard; DNA; 17 BP.
 XX
 AC AA293921;
 XX
 DT 25-SEP-2000 (first entry)

XX Primer (EP1/11RT) for amplifying EP-1 prostaglandin receptor sequence.
 DE
 XX Prostaglandin; receptor; pulmonary system; glaucoma; identification;
 KW allele; polymorphism; detection; prostanoic; EP; IP; DP; EP; TP; human;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200029614-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 12-NOV-1998; 98WO-IB001803.
 XX
 PR 12-NOV-1998; 98WO-IB001803.
 XX
 XX (EURO-) EUROPA MEDICAL AB.
 PA
 XX Jonsson L, Lindstrom HR;
 PI WPI; 2000-387820/33.
 XX
 DR Assessing prostanoic response status in an individual suffering from
 PT prostaglandin associated diseases such as pulmonary hypertension,
 PT glaucoma or arteriosclerosis, comprises comparing polymorphic patterns.
 XX
 PS Disclosure; Page 38; 57pp; English.
 XX
 CC The prostaglandin receptor family encompasses at least five classes of
 CC receptors designated EP, EP, IP, DP and TP receptors which are classified
 CC based on their sensitivity to the five primary prostanoic (E2alpha, E2,
 CC I2, D2 and TXA2). EP receptors further comprise four subtypes,
 CC designated EP1-4, which differ in their responses to various agonists and
 CC antagonists. The receptors have also shown a degree of cross reactivity.
 CC They may derive from a common ancestral gene. All of the receptors may
 CC exist as allelic variants and these polymorphisms may have an effect on a
 CC patients reaction to prostanoic. Detection of these polymorphisms may
 CC identify patients at risk from toxic or abnormal responses to prostanoic
 CC treatment. The prostaglandins play a role in the pulmonary system and in
 CC glaucoma. Fourteen primers (See AA293918-293931) were used to amplify the
 CC EP-1 prostaglandin receptor sequence. This primer corresponds to the 5'
 CC region and nucleotides 1-12 of the EP-1 receptor sequence. Primers whose
 CC designation include a "r" have the 29 base "tail sequence" given in
 CC GENESQ record AA293932 added to their 5' end
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 12 CTCTGCCCGCTGTGCT 28
 Db |||||
 17 CTCTGCCCGCTGTGCT 1
 RESULT 170
 AAC61360/c
 ID AAC61360 standard; DNA; 17 BP.
 XX
 AC AAC61360;
 XX
 XX 30-JAN-2001 (first entry)
 DT
 XX Human EP and EP1 receptor genes PCR primer SEQ ID NO: 160.
 DE Human; genetic polymorphism; disease diagnosis; treatment; cancer;
 KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200056922-A2.
 PN

XX PD 28-SEP-2000.
 XX PF 23-MAR-2000; 2000WO-GB001102.
 XX PR 23-MAR-1999; 99US-0126046P.
 XX PR 23-MAR-1999; 99WO-IB000497.
 XX PR 24-MAR-1999; 99US-0126243P.
 XX PR 23-DEC-1999; 99US-00471890.
 XX PA (GEMI-) GEMINI GENOMICS AB.
 XX PI Lindstrom PHR, Norberg LT, Jonsson L, Olaiisson E, Sanders R;
 XX DR WPI; 2000-638268/61.
 XX SQ Sequence 17 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 12 CTCGCGCCGCTGCTGCT 28
 Db 17 CTGTGCCCGCTGCTGCT 1
 RESULT 171
 AAF02125/C
 ID AAF02125 standard; DNA; 17 BP.
 XX AC AAF02125;
 XX DT 16-FEB-2001 (first entry)
 XX DE Hammerhead ribozyme substrate #420.
 XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 XX KW interferon alpha; ss.
 XX OS Homo sapiens.
 XX PN WO2000061729-A2.
 XX PD 19-OCT-2000.
 XX PF 11-APR-2000; 2000WO-US009721.
 XX PR 12-APR-1999; 99US-0129390P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX DR WPI; 2000-647423/62.

PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 XX interferon alpha and erythropoietin.
 XX Claim 37; Page 65; 164pp; English.
 XX The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX SQ Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 49 CCTGAGAACACAGCCTG 65
 Db 17 CCTGAGAACACAGCCTG 1
 RESULT 172
 ABL46462
 ID ABL46462 standard; RNA; 17 BP.
 XX AC ABL46462;
 XX DT 27-JUN-2003 (first entry)
 XX DE Human GR1D hammerhead ribozyme substrate oligonucleotide #95.
 XX KW Human; Grb2-related with Insert Domain; GR1D; T-cell;
 XX KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 XX KW leukaemia; cytostatic; ss.
 XX OS Homo sapiens.
 XX PN WO200162911-A2.
 XX PD 30-AUG-2001.
 XX PF 23-FEB-2001; 2001WO-US005957.
 XX PR 24-FEB-2000; 2000US-0184594P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX DR WPI; 2001-550088/61.
 XX PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX PT (GR1D) gene comprises using antisense and enzymatic nucleic acid
 XX PT molecules such as hammerhead ribozymes.
 XX PS Claim 4; Page 61; 108pp; English.
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GR1D) gene. GR1D is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GR1D, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX SQ Sequence 17 BP; 2 A; 6 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 1.2e+02;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1562 GGACCTCTCCACCTCTG 1578
 DB 1 GGACUUCUCCAUUCUG 17

RESULT 173
 AAH80102/c
 ID AAH80102 standard; cDNA; 17 BP.
 XX
 AC
 XX
 XX
 DT 19-SEP-2001 (first entry)
 XX
 DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 66.
 XX
 KW Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW disease diagnosis; ss.
 XX
 OS Oryctolagus cuniculus.
 XX
 PN US6251588-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 10-FEB-1998; 98US-00021701.
 XX
 PR 10-FEB-1998; 98US-00021701.
 XX
 PA (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 PI Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 XX
 DR WPI; 2001-424456/45.
 XX
 XX Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters.
 XX
 PS Example 1; Col 47; 342pp; English.
 XX
 CC The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridize to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridisable
 CC to the target nucleotide sequence. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTGGGGTCTCTGCCC 19
 DB 17 GTCTGGGGTCTCTGCCC 1

RESULT 174
 ABN06570
 ID ABN06570 standard; DNA; 17 BP.
 XX
 AC ABN06570;
 XX

DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6562.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US016981.
 XX
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (ABOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;
 XX
 DR WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 6562; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 8 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1502 AACCAAGAGGAGGAGC 1518
Db 1 AGCCAAAGAGGAGGAGC 17
|||||

RESULT 177
ABN08675
ID ABN08675 standard; DNA; 17 BP.
XX AC ABN08675;
XX
XX 29-MAY-2002 (first entry)
DT
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8667.
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; Gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
OS
FN WO200192524-A2.
XX
XX 06-DEC-2001.
PD
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207458P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0268860P.
XX
XX (AEOM-) AEOMICA INC.
PA
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT

PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 8667; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 9 A; 2 C; 6 G; 0 T; 0 U; 0 Other;
SQ

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1501 AACCAAGAGGAGGAGC 1517
Db 1 AGCCAAAGAGGAGGAGC 17
|||||

RESULT 178
ABQ63445
ID ABQ63445 standard; DNA; 17 BP.
XX AC ABQ63445;
XX
XX 20-AUG-2002 (first entry)
DT
DE Human KTOM1a portion (ABQ63232) probe # 158.
XX
XX Human; KTOM1a; KTOM1; kidney tumour overexpressed membrane; cytostatic;
KW gene therapy; cancer; kidney; liver; bone marrow; brain; heart; lung;
KW kidney; colon; skeletal muscle; testis; uterus; placenta; probe; ss.
XX
XX Homo sapiens.
OS
PN WO200224750-A2.
XX
XX 28-MAR-2002.
PD
XX 21-SEP-2001; 2001WO-US029656.
XX
XX 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR

PR 23-MAY-2001; 2001US-00864761.
PR 28-AUG-2001; 2001US-0315676P.
XX (AEOM-) AEOMICA INC.
XX Zhang J;
XX WPI; 2002-479509/51.
XX
XX New human kidney tumor overexpressed membrane (KTOM1) protein and nucleic
PT acids encoding the protein, useful for treating subjects having defects
PT in KTOM1 which can manifest as cancer of the kidney, or as a disorder of
PT e.g., liver or bone.
XX
XX Example 2; Page 178; 418pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding human
CC KTOM1 (kidney tumor overexpressed membrane) protein. The protein of the
CC invention has cytostatic activity. The nucleotide may have a use in gene
CC therapy. The KTOM1 nucleic acids may be used to diagnose, treat or
CC monitor a disease caused by altered expression of human KTOM1.
CC Compositions comprising the nucleic acids, proteins or antibodies may be
CC used to treat subjects having defects in KTOM1 which can manifest as
CC cancer of the kidney, as well as a disorder of liver, bone marrow, brain,
CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
CC function. The sequence represents a probe used in the invention to scan
CC the nt 1-1001 portion of human KTOM1a (AB063232)
XX
SQ Sequence 17 BP; 3 A; 9 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1583 CCTGCTGAGTCCCTCCAC 1599
Db 1 CCTGCTGACTCCACAC 17
RESULT 179
ABV79342
ID ABV79342 standard; DNA; 17 BP.
XX
AC ABV79342;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 588.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000653.
PR 30-JAN-2001; 2001WO-US000654.
PR 30-JAN-2001; 2001WO-US000655.
PR 30-JAN-2001; 2001WO-US000656.
PR 30-JAN-2001; 2001WO-US000657.
PR 30-JAN-2001; 2001WO-US000658.
PR 30-JAN-2001; 2001WO-US000659.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX

PI Zhan J;
XX
DR WPI; 2002-675582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 140; 718pp; English.
PS
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 8 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1456 AAGAGAAAGACCCAGAG 1472
Db 1 AAGAGGAGAGACCTAGAG 17
RESULT 180
ABV79344
ID ABV79344 standard; DNA; 17 BP.
XX
AC ABV79344;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 590.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
PA (AEOM-) AEOMICA INC.
XX

```

PA (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
XX
XX Example 2; Page 141; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL), see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention
XX
XX Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1458 GAGGAAGACCCAGAGGA 1474
DB 1 GAGGAAGACCTAGAGGA 17
RESULT 181
ABV79345
ID ABV79345 standard; DNA; 17 BP.
XX
XX AC ABV79345;
XX
XX 03-JAN-2003 (first entry)
XX
XX Human HTPL scanning oligonucleotide SEQ ID 591.
XX
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
XX
XX EP1229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 23-MAY-2001; 2001US-00864761.
PR

```



```

XX OS Homo sapiens.
XX PN WO200186124-A2.
XX PD 22-NOV-2001.
XX PF 16-MAY-2001; 2001WO-US015866.
XX PR 16-MAY-2000; 2000US-00572021.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (GLAX) GLAXO GROUP LTD.
XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX WPI; 2002-082995/11.
XX PT Novel polynucleotide which down regulates expression of Ets-related gene,
XX useful for treating cancer, diabetic retinopathy, macular degeneration,
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX PS Claim 4; Page 73; 149pp; English.
XX PT The invention relates to a nucleic acid molecule (I) which down regulates
XX expression of an Ets-related gene (ERG). (I) is useful for treating
XX conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
XX tumour angiogenesis, diabetic retinopathy, macular degeneration, verruca
XX neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
XX vulgaris, angiofibroma of tubercous sclerosis, port-wine stains, Sturge
XX Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
XX syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
XX treating a patient having a condition associated with the level of ERG,
XX by contacting cells of the patient with (I) under conditions suitable for
XX the treatment. The method comprises the use of one or more therapies
XX under conditions suitable for the treatment. Leukaemia or tumour
XX angiogenesis is treated by administering (I) to the patient in
XX conjunction with one or more of other therapies such as radiation or
XX chemotherapy treatment. (I) is useful for reducing ERG activity in a
XX cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
XX ERG gene, by contacting (I) with RNA, in the presence of a divalent
XX cation such as Mg2+. (I) is useful for diagnosis of conditions and
XX diseases related to the expression of ERG, and as diagnostic tool to
XX examine genetic drift and mutations within diseased cells or to detect
XX the presence of ERG RNA in a cell. (I) is useful for specifically
XX targeting genes that share homology with ERG gene or ERG fusion genes.
XX ABK17354-ABK22719 represent nucleic acids, including antisense and
XX enzymatic nucleic acid molecules which regulate expression of ERG, and
XX related PCR primers of the invention
XX SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;
      Query Match 0.9%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 58.8%; Pred. No. 1.2e+02;
      Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 142 TCCTGTTACTACTAGC 158
DB 1 UCCGUUACUACUAGC 17

RESULT 185
ABN85838
ID ABN85838 standard; DNA; 17 BP.
XX AC ABN85838;
XX DT 03-SEP-2002 (first entry)
XX DE Related to Bombyx mori silk fibroin primer #38.
XX KW Silk; fibroin; textile industry; PCR; primer; ss.
XX PT

XX OS Unidentified.
XX PN WO200240528-A1.
XX PD 23-MAY-2002.
XX PF 26-OCT-2001; 2001WO-CN001506.
XX PR 26-OCT-2000; 2000CN-00125859.
XX PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
XX PI Lu C, Huang J, Zhao Y, Zhang F, Chen X;
XX WPI; 2002-427084/45.
XX PT Method for producing non-natural silk by Bombyx mori with modifying heavy
XX and light chains of fibroin in natural silk by DNA recombination
XX technology and protein engineering, applicable in sericulture and textile
XX industry.
XX PS Example 3; Page 18; 50pp; Chinese.
XX PT This invention relates to a silk which constitutes recombinant Bombyx
XX mori silk fibroin obtained by modification or variation at the heavy or
XX light chains of the fibroin. The method is for producing non-natural
XX silk, which is applicable in sericulture and textile industry. Such
XX modified silk has improved performance. The present sequence is a primer
XX related to the invention
XX SQ Sequence 17 BP; 4 A; 2 C; 7 G; 4 T; 0 U; 0 Other;
      Query Match 0.9%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 88.2%; Pred. No. 1.2e+02;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 800 CGGGATTGATGACGAGT 816
DB 1 CAGGGTTGATGACGAGT 17

RESULT 186
ABL31482/C
ID ABL31482 standard; DNA; 17 BP.
XX AC ABL31482;
XX DT 21-MAR-2002 (first entry)
XX DE Human HLA genotyping oligonucleotide SEQ ID NO 971.
XX KW Human; human leukocyte antigen; HLA; genotype; polymorphism;
XX immunogenetic; transplantation; genetic disease; ss.
XX OS Homo sapiens.
XX PN WO200192572-A1.
XX PD 06-DEC-2001.
XX PF 01-JUN-2001; 2001WO-JP004662.
XX PR 01-JUN-2000; 2000JP-00164798.
XX PA (NTSN) NISSHINBO IND INC.
XX PA (SYST-) SYSTEM RES INC.
XX PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
XX WPI; 2002-122074/16.
XX DE Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
XX individuals e.g. by determining immunogenetic differences when
XX PT

```

PT transplanting between them.
XX
PS Claim 10; Page 277; 345pp; Japanese.
XX
CC The invention relates to a typing kit for judging human leukocyte antigen
CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base
CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of
CC genes e.g. belonging to HLA class I antigens on human genome and
CC containing gene polymorphisms as alloantigens have been immobilised as
CC primers for amplification of cleaved nucleic acids relating to gene
CC polymorphisms. The method is useful for judging HLA genotypes of
CC individuals by determining immunogenetic differences before transplanting
CC between them, providing genetic information to decide compatibility of
CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,
CC pancreas, Langerhans islet in pancreas and cornea, susceptibility
CC diagnosis of genetic diseases and identifying individuals
XX
SQ Sequence 17 BP; 4 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 38 CACTCGGTCATCCTGAG 54
|||||
Db 17 CACTCGGTCAGCCTGTG 1
RESULT 187
ID ABK55737/C
AC ABK55737 standard; RNA; 17 BP.
AC
AC ABK55737;
XX
DT 02-JUL-2002 (first entry)
DE Human CLCA1 gene enzymatic nucleic acid #108.
XX
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW anti-inflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; mucokinetic;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
XX Homo sapiens.
XX
XX WO200211674-A2.
PN 14-FEB-2002.
PD
XX
XX 09-AUG-2001; 2001WO-US024970.
PF
XX
XX 09-AUG-2000; 2000US-0224383P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
PI
XX
XX WPI; 2002-217145/27.
DR
XX
XX Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
PT
XX
XX Claim 4; Page 54; 152pp; English.
PS
XX
XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic

CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 2 A; 3 C; 3 G; 0 T; 9 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 374 CAAGCAGATGCAGAGAT 390
|||||
Db 17 CAACAGATACAGAGAT 1
RESULT 198
ID ABT21381/C
AC ABT21381 standard; DNA; 17 BP.
AC
AC ABT21381;
XX
DT 16-APR-2003 (first entry)
XX
DE Multiplex group PCR primer #128.
XX
XX Racing potential; horse; grandpaternal DNA; over-represented; breeding;
KW grandmother; performance; progeny horse; PCR; primer; ss.
XX
XX Unidentified.
OS
XX WO200292851-A2.
PN
XX 21-NOV-2002.
PD
XX
XX 15-MAY-2002; 2002WO-GB002273.
PF
XX
XX 15-MAY-2001; 2001GB-00011886.
PR
XX
XX (ANIM-) ANIMAL HEALTH TRUST.
PA (BRHO-) BRITISH HORSERACING BOARD.
XX
XX Binns MM, Swinburne JE;
PI
XX WPI; 2003-129314/12.
DR
XX
XX Determining the racing potential of a horse comprises measuring whether
PT grandpaternal or grandmaternal DNA from the selected grandmother DNA is
PT over-represented in the genome of the horse.
XX
XX Example 2; Page 24; 49pp; English.
PS
XX
XX The invention relates to a novel method for determining racing potential
CC of a horse. The method comprises measuring: whether grandpaternal DNA is
CC over-represented in the genome of the horse; or in the case where one of
CC the grandmothers was selected for breeding on the basis of racing
CC performance, whether grandmaternal DNA from the selected grandmother is
CC over-represented in the genome of the horse which indicates that the
CC horse has good racing potential. The method of the invention is useful
CC for determining the racing potential of a horse or for obtaining a
CC progeny horse with good racing potential. This polynucleotide sequence
CC represents a PCR primer used in the detection method of over-
CC representation of DNA from male grandparents of the invention
XX

```
SQ Sequence 17 BP; 4 A; 3 C; 9 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 GTGCTGCTCTCCAC 40
Db 17 GTCTGCTCTCCAC 1

RESULT 189
ABZ65102
ID ABZ65102 standard; RNA; 17 BP.
XX AC ABZ65102;
XX DT 21-MAR-2003 (first entry)
XX DE Human HER2 DNzyme substrate #559.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.
XX OS Homo sapiens.
XX PN WO200297114-A2.
XX PD 05-DEC-2002.
XX PF 29-MAY-2002; 2002WO-US016840.
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Mcswiggen J;
XX DR WPI; 2003-140484/13.
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX PS Claim 4; Page 143; 185pp; English.
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX CC rheumatic activity. The nucleic acid molecules are useful for reducing
XX CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX CC also useful for treating breast, ovarian, colorectal, lung, prostate,
XX CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX CC ribozymes of the invention
XX SQ Sequence 17 BP; 5 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.8%; Pred. No. 1.2e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1315 ACAAGGCGATCTCGATC 1331
Db 1 ACAAGGCGAUCUGGATC 17

RESULT 191
ABZ61695
ID ABZ61695 standard; RNA; 17 BP.
XX AC ABZ61695;
XX DT 21-MAR-2003 (first entry)
XX DE Human H-Ras DNzyme target #486.
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
```

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.

XX WO200297114-A2.
XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-US016940.
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.

XX (RIBO-) RIBOZYME PHARM INC.
XX Mcswiggen J;
XX WPI; 2003-140484/13.

XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 120; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention

XX Sequence 17 BP; 3 A; 4 C; 5 G; 0 T; 5 U; 0 Other;
XX Query Match 0.9%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 64.7%; Pred. No. 1.2e+02;
XX Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 658 TGAAGAGGCTTCTAC 674
DB 1 UGAGGAGGCTTCTAC 17

RESULT 192
ACD62482
ID ACD62482 standard; RNA; 17 BP.

XX ACD62482;
XX 23-SEP-2003 (first entry)
XX HCV minus strand DNzyme substrate sequence #569.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNzyme; zinczyme;
XX ambrzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.
XX WO200281494-A1.

XX 17-OCT-2002.
XX 26-MAR-2002; 2002WO-US009187.
XX 26-MAR-2001; 2001US-00817879.
XX 08-JUN-2001; 2001US-00877478.
XX 08-JUN-2001; 2001US-0296876P.
XX 24-OCT-2001; 2001US-0335059P.
XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PVC/) PAVCO P.
XX (LEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.

XX Claim 1; Page 285; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
XX inozymes, zinczymes, ambrzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNzyme or minus strand DNzyme sequences disclosed in the present
XX invention

XX Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;
XX Query Match 0.9%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 76.5%; Pred. No. 1.2e+02;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 291 GCTGAGGAGATGACCAA 307
DB 1 GCTGAGGAGGCTGACCAA 17

RESULT 193
ACD60187/c
ID ACD60187 standard; RNA; 17 BP.

XX ACD60187;
XX 24-SEP-2003 (first entry)
XX HCV DNzyme substrate sequence #1709.
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX WO200281494-A1.
 XX 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Claim 1; Page 264; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX Sequence 17 BP; 2 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 0.98; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 292 CTGAGGAGATGACCAAG 308
 Db 17 CTGAGGAGCTGGCAAG 1

RESULT 194
 ACD65057
 ID ACD65057 standard; RNA; 17 BP.
 XX
 AC ACD65057;
 AC
 DT 30-SEP-2003 (first entry)
 XX
 DE HCV minus strand DNazyme substrate sequence #1856.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX WO200281494-A1.
 XX 17-OCT-2002.
 XX 26-MAR-2002; 2002WO-US009187.
 XX 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEP/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Claim 1; Page 308; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention

CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNase or minus strand DNase sequences disclosed in the present
CC invention
XX
SQ Sequence 17 BP; 3 A; 2 C; 6 G; 0 T; 6 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1154 CAATATGACTACCCAGA 1170
DB 17 CAATATGACTACCCAGA 1
RESULT 195
ACD51143/C
ID ACD51143 standard; RNA; 17 BP.
XX ACD51143;
AC ACD51143;
DT 23-SEP-2003 (first entry)
XX HBV hammerhead ribozyme substrate sequence #405.
DE
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNase; zymase;
KW ambery; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
OS Hepatitis B virus.
XX
PN WO200281494-A1.
XX
XX 17-OCT-2002.
PD
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.

SQ Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.2e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1267 AGGACGCCATCCCTGAG 1283
DB 1 AGGACCCACCCCTGAG 17
RESULT 195
ACD52411/C
ID ACD52411 standard; RNA; 17 BP.
XX ACD52411;
AC ACD52411;
DT 23-SEP-2003 (first entry)
XX HCV minus strand DNase substrate sequence #554.
DE
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNase; zymase;
KW ambery; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
OS Hepatitis C virus.
XX
PN WO200281494-A1.
XX
XX 17-OCT-2002.
PD
XX 26-MAR-2002; 2002WO-US009187.
XX
XX 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
PS Claim 1; Page 284; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNases,
CC inozymes, zymases, ambery, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV

XX PS Example 1; Page 144; 387pp; English.

XX CC The present invention relates to nucleic acid molecules which modulate

XX CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

XX CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

XX CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

XX CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

XX CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

XX CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

XX CC as oligonucleotides that specifically bind the Enhancer I region of HBV

XX CC DNA. The nucleic acids may be used to modulate the expression of HBV

XX CC genes and HBV viral replication. Also disclosed is a method for screening

XX CC compounds and/or potential therapies directed against HBV, and compounds

XX CC that modulate the expression and/or replication of HCV. The compounds and

XX CC methods of the invention are useful for the treatment of degenerative and

XX CC disease states related to HBV and HCV infection, replication and gene

XX CC expression such as cirrhosis, liver failure, and hepatocellular

XX CC carcinoma. The present sequence represents a substrate for one of the HBV

XX CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences

XX CC disclosed in the present invention

XX SQ Sequence 17 BP; 1 A; 5 C; 2 G; 0 T; 9 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1513 AGAAGCCAGAGCCAAA 1529

DB 17 AGAAGTCAGAGCCAAA 1

RESULT 197

ID ACD60202 standard; RNA; 17 BP.

XX AC ACD60202;

XX DT 24-SEP-2003 (first entry)

XX DE HCV DNazyme substrate sequence #1724.

XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;

XX KW RNA stability; RNA expression; RNA synthesis; antisense;

XX KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;

XX KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;

XX KW HBV reverse transcriptase; Enhancer I region; viral replication;

XX KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;

XX KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;

XX KW virucide; antiinflammatory; substrate; ss.

XX OS Hepatitis C virus.

XX PN WO200281494-A1.

XX PD 17-OCT-2002.

XX PF 26-MAR-2002; 2002WO-US009187.

XX PR 26-MAR-2001; 2001US-00817879.

XX PR 08-JUN-2001; 2001US-00877478.

XX PR 08-JUN-2001; 2001US-0296876P.

XX PR 24-OCT-2001; 2001US-0335059P.

XX PR 05-DEC-2001; 2001US-0337055P.

XX PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (NACE/) NACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

XX PI Draper K, Roberts E;

XX WI; 2003-229207/22.

XX PT Novel compound useful for treating cirrhosis, liver failure,

XX PT hepatocellular carcinoma, or condition associated with hepatitis C virus

XX PT infection.

XX PS Claim 1; Page 264; 387pp; English.

XX CC The present invention relates to nucleic acid molecules which modulate

XX CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

XX CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

XX CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

XX CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed

XX CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

XX CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

XX CC as oligonucleotides that specifically bind the Enhancer I region of HBV

XX CC DNA. The nucleic acids may be used to modulate the expression of HBV

XX CC genes and HBV viral replication. Also disclosed is a method for screening

XX CC compounds and/or potential therapies directed against HBV, and compounds

XX CC that modulate the expression and/or replication of HCV. The compounds and

XX CC methods of the invention are useful for the treatment of degenerative and

XX CC disease states related to HBV and HCV infection, replication and gene

XX CC expression such as cirrhosis, liver failure, and hepatocellular

XX CC carcinoma. The present sequence represents a substrate for one of the HCV

XX CC DNazyme or minus strand DNazyme sequences disclosed in the present

XX CC invention

XX SQ Sequence 17 BP; 5 A; 7 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 70.6%; Pred. No. 1.2e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1153 CCAATATGACTAACCG 1169

DB 1 CCAAUAGACUCCCCAG 17

RESULT 198

ACC63240/C

ID ACC63240 standard; DNA; 17 BP.

XX AC ACC63240;

XX DT 01-JUL-2003 (first entry)

XX DE Murine oligonucleotide associated with tumour supression, SEQ ID 487.

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;

XX KW tumour supression; tumour reversion; apoptosis; virus resistance;

XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;

XX KW schizoprenia; ss.

XX OS Mus musculus.

XX PN WO2003025176-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004210.

XX PR 17-SEP-2001; 2001FR-00011979.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-333167/31.
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 88; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC6806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 30 CTGTCTCCCACTCGTC 46
 Db 17 CTGTCTCCGACTCGATC 1
 RESULT 199
 ACC68438
 ID ACC68438 standard; DNA; 17 BP.
 AC ACC68438;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5685.
 XX
 CC Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; ss;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Anson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 CC New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 695; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC6806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a

CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 4 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1328 GATCTGCTCCCTCGACA 1344
 Db 1 GATCTGCTCATTGACA 17
 RESULT 200
 ADB42595/c
 ID ADB42595 standard; DNA; 17 BP.
 XX
 AC ADB42595;
 XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #2918.
 XX
 CC Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Anson R, Tuijnder M;
 XX
 DR WPI; 2003-441574/41.
 XX
 CC New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 PS Disclosure; Page 373; 771pp; French.
 XX
 CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and/or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 717 GAGTACTTCCAGGAGC 733
DB 17 GAGAACTTCCAGGATC 1
RESULT 201
ADB42646/C
ID ADB42646 standard; DNA; 17 BP.
XX
AC ADB42646;
XX
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #2969.
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-18004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
PT
PS Disclosure; Page 379; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 717 GAGTACTTCCAGGAGC 733
DB 17 GAGAACTTCCAGGATC 1
RESULT 202
ADB42646/C
ID ADB42646 standard; DNA; 17 BP.
XX
AC ADB42646;
XX
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Human Na/H exchanger-like protein 1 gene oligonucleotide #1289.
XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW NHELP1; passive replacement therapy; vaccine; diagnosis.
XX
XX Homo sapiens.
XX EP1273660-A2.
XX
XX 08-JAN-2003.
XX
XX 25-JAN-2002; 2002EP-00001160.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX 23-MAY-2001; 2001US-00864761.
XX 21-DEC-2001; 2001US-0343331P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y;
XX
XX WPI; 2003-302724/30.
XX
XX New human sodium-hydrogen exchanger like protein 1 (NHELP1), useful as a
PT passive replacement therapy or as a vaccine for treating or preventing
PT disorders associated with aberrant expression or activity of human
PT NHELP1.
XX
XX Example 2; SEQ ID NO 1329; 468pp; English.
XX
XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC exchanger like protein (NHELP1). The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHELP1 nucleic acid molecule, NHELP1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHELP1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHELP1. The NHELP1 nucleic acid
CC or protein is useful as passive replacement therapy, as a vaccine, or in
CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
CC spanning the sequence of the human NHELP1 gene (ADC03514).
XX
XX Sequence 17 BP; 0 A; 11 C; 0 G; 6 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1381 AAGAGGAGGAGAGGGG 1397
DB 17 AGGAGGAGGAGAGGGG 1

```

RESULT 203
ID ADD80993 standard; DNA; 17 BP.
XX AC
XX ADD80993;
XX DT
XX 29-JAN-2004 (first entry)
XX DE
XX Rabbit beta-globin fragment derived oligonucleotide #27.
XX ss; oligonucleotide hybridisation potential; efficient hybridisation;
XX large array; minimum oligonucleotide synthesis; rabbit; beta-globin.
XX OS
XX Oryctolagus cuniculus.
XX PN
XX US2003054346-A1.
XX PD
XX 20-MAR-2003.
XX PF
XX 15-FEB-2001; 2001US-00784674.
XX PR
XX 10-FEB-1998; 98US-00021701.
XX (SHAN/) SHANNON K W.
XX (WOLB/) WOLBER P K.
XX (DELE/) DELENSTARR G C.
XX (WEBB/) WEBB P G.
XX (KINC/) KINCAID R H.
XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
XX WPI; 2003-743746/70.
XX Predicting potential of oligonucleotides to hybridize to target
XX nucleotide sequence comprises determining and evaluating for each
XX oligonucleotide a parameter predictive of the oligonucleotides ability to
XX hybridize with target.
XX Example 1; SEQ ID NO 66; 423bp; English.
XX The invention relates to a method of predicting the potential of
XX oligonucleotides to hybridize to target nucleotide sequences. The method
XX is useful for predicting the potential of an oligonucleotide to hybridise
XX to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
XX contains chemically modified nucleotides. The method is also useful for
XX predicting the potential of the oligonucleotides to hybridise to a
XX complementary target nucleotide sequence. The method is useful to predict
XX efficient hybridisation oligonucleotides for each of multiple target
XX sequences therefore very large arrays may be constructed and tested with
XX minimum synthesis of oligonucleotides. The present sequence represents a
XX rabbit beta-globin derived oligonucleotide sequence.
XX SQ Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GTCGCGGTCCTGCCC 19
DB 17 GTCGCGGTCCTGCCC 1
RESULT 204
AAF48241/c
ID AAF48241 standard; DNA; 15 BP.
XX AC
XX AAF48241;
XX 30-MAR-2001 (first entry)
XX DT
XX IGFBP3 oligonucleotide #1661.
XX DE
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200078341-A1.
XX PD
XX 28-DEC-2000.
XX PF
XX 21-JUN-2000; 2000WO-AU000693.
XX PR
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX Example 7; Page 55; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation.
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX SQ Sequence 15 BP; 2 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1376 TTCTGAAGAGGAGGG 1390
DB 15 TTCTGAAGAGGAGGG 1
RESULT 205
AAF45342
ID AAF45342 standard; DNA; 15 BP.
XX AC
XX AAF45342;
XX 30-MAR-2001 (first entry)
XX DT
XX IGFBP2 oligonucleotide #181.
XX DE
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX

```

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PP
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PR
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antiseptic nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX
 XX Example 6; Page 35; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antiseptic oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antiseptic
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 0 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 18 CCGCTGCTGCTGCTG 32
 DQ ||||| |||||
 DB 1 CCGCTGCTGCTGCTG 15
 RESULT 206
 AAF49639
 ID AAF49639 standard; DNA; 15 BP.
 XX
 XX AAF49639;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #599.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 PF
 XX 21-JUN-1999; 99US-0140345P.
 PP
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PR
 XX Wright CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antiseptic nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX
 XX Example 8; Page 64; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antiseptic oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antiseptic
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1504 CCAAGGAGGAGGAGC 1518
 DQ ||||| |||||
 DB 1 CCATGGAGGAGGAGC 15
 RESULT 207
 AAF49640
 ID AAF49640 standard; DNA; 15 BP.
 XX
 XX AAF49640;
 AC
 XX 30-MAR-2001 (first entry)
 DT
 XX IGF-I oligonucleotide #600.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS
 XX WO200078341-A1.
 PN

```

XX PD      28-DEC-2000.
XX PF      21-JUN-2000; 2000WO-AU000693.
XX PR      21-JUN-1999; 99US-0140345P.
XX PA      (MURD-) MURDOCH CHILDRENS RES INST.
XX PI      Wright CJ, Werther GA, Edmondson SR;
XX DR      WPI; 2001-041421/05.
XX PT      Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT      UV (ultra-violet) treatment (optional) and an antisenesc nucleic acid that
XX PT      inhibits or reduces growth factor mediated cell proliferation and/or
XX PS      inflammation.
XX PS      Example 8; Page 64; 201pp; English.
XX CC      The present invention relates to a method for ameliorating the effects of
XX CC      skin disorders. The method comprises contacting the skin with an
XX CC      antisenesc oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC      receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC      inhibiting or reducing growth factor mediated cell proliferation,
XX CC      inflammation and/or other disorders. The present sequence is an
XX CC      oligonucleotide which can be used to design the antisenesc
XX CC      oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC      F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC      ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC      neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC      hyperneovascular condition such as a neovascular condition of the retina,
XX CC      brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC      disease, kidney disease, hyperproliferation of the inside of blood
XX CC      vessels or any other hyperplasia
XX SQ      Sequence 15 BP; 5 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
          Query Match      0.8%; Score 13.4; DB 1; Length 15;
          Best Local Similarity 93.3%; Pred. No. 1.1e+02;
          Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1505 CAAGGAGGAGGAGCC 1519
Db      1 CATGGAGGAGGAGCC 15

RESULT 208
AAF49372/C
ID      AAF49372 standard; DNA; 15 BP.
XX AC      AAF49372;
XX DT      30-MAR-2001 (first entry)
XX DE      IGF-I oligonucleotide #332.
XX KW      Antisenesc therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW      cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW      skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW      IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW      growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW      keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW      hyperneovascular condition; hyperplasia; kidney disease;
XX OS      Homo sapiens.
XX PN      WO200078341-A1.
XX PD      28-DEC-2000.
XX PR      21-JUN-2000; 2000WO-AU000693.
XX PA      (MURD-) MURDOCH CHILDRENS RES INST.

```

```

XX PR      21-JUN-1999; 99US-0140345P.
XX PA      (MURD-) MURDOCH CHILDRENS RES INST.
XX PI      Wright CJ, Werther GA, Edmondson SR;
XX DR      WPI; 2001-041421/05.
XX PT      Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX PT      UV (ultra-violet) treatment (optional) and an antisenesc nucleic acid that
XX PT      inhibits or reduces growth factor mediated cell proliferation and/or
XX PS      inflammation.
XX PS      Example 8; Page 63; 201pp; English.
XX CC      The present invention relates to a method for ameliorating the effects of
XX CC      skin disorders. The method comprises contacting the skin with an
XX CC      antisenesc oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX CC      receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX CC      inhibiting or reducing growth factor mediated cell proliferation,
XX CC      inflammation and/or other disorders. The present sequence is an
XX CC      oligonucleotide which can be used to design the antisenesc
XX CC      oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX CC      F45161). The method is useful for ameliorating the effects of psoriasis,
XX CC      ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX CC      neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX CC      hyperneovascular condition such as a neovascular condition of the retina,
XX CC      brain or skin, growth factor-mediated malignancies, other sclerotic
XX CC      disease, kidney disease, hyperproliferation of the inside of blood
XX CC      vessels or any other hyperplasia
XX SQ      Sequence 15 BP; 2 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
          Query Match      0.8%; Score 13.4; DB 1; Length 15;
          Best Local Similarity 93.3%; Pred. No. 1.1e+02;
          Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1361 GGAGAGGAGTCTCCGA 1375
Db      15 GGAGAGGAGTCTCCGA 1

RESULT 209
AAF52624
ID      AAF52624 standard; DNA; 15 BP.
XX AC      AAF52624;
XX DT      30-MAR-2001 (first entry)
XX DE      IGF-I oligonucleotide #3584.
XX KW      Antisenesc therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX KW      cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX KW      skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX KW      IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX KW      growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX KW      keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX KW      hyperneovascular condition; hyperplasia; kidney disease;
XX OS      Homo sapiens.
XX PN      WO200078341-A1.
XX PD      28-DEC-2000.
XX PR      21-JUN-2000; 2000WO-AU000693.
XX PA      (MURD-) MURDOCH CHILDRENS RES INST.

```

XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 8; Page 84; 20lpp; English.
 PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 2 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1584 CTGCTGAGTCCCTCA 1598
 DB 1 CTGCTGAGTCCCTCA 15
 RESULT 210
 AAF53134
 ID AAF53134 standard; DNA; 15 BP.
 XX AAF53134;
 AC AAF53134;
 XX 30-MAR-2001 (first entry)
 DT IGF-I oligonucleotide #4094.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 8; Page 87; 20lpp; English.
 PS The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 4 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
 SQ Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1393 AGGGGGCGCCGACAGA 1407
 DB 1 ACGGGGCGCCGACAGA 15
 RESULT 211
 AAF49638
 ID AAF49638 standard; DNA; 15 BP.
 XX AAF49638;
 AC AAF49638;
 XX 30-MAR-2001 (first entry)
 DT IGF-I oligonucleotide #598.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

PT inflammation.
 XX Example 8; Page 64; 201pp; English.
 PS
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 6 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1503 ACCAAGGAGGAGAG 1517
 DB 1 ACCATGGAGGAGAG 15
 RESULT 212
 ABK81387
 ID ABK81387 standard; DNA; 15 BP.
 XX
 AC ABK81387;
 DT 13-AUG-2002 (first entry)
 XX
 DE SCVA21 gene allele specific oligonucleotide primer #1.
 KW Small inducible cytokine subfamily A (Cys-Cys) member 21; SCVA21;
 KW polymorphism; haplotype; immunological disorder; gene expression;
 KW drug development; immunomodulator; allele specific oligonucleotide;
 KW primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200232930-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 09-OCT-2001; 2001WO-US046141.
 XX
 PR 19-OCT-2000; 2000US-0241622P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Bentivegna SC, Russo DP;
 XX
 DR WPI; 2002-435528/46.
 XX
 PT New genetic variants comprising haplotypes of the small inducible
 PT cytokine subfamily A, member 21 (SCVA21) gene, useful in improving the
 PT efficiency of screening for drugs for treating immunological disorders or
 PT for targeting SCVA21.
 XX
 PS Claim 14; Page 13; 56pp; English.
 XX
 CC The invention describes an isolated polynucleotide, which comprises genes
 CC and haplotypes of the small inducible cytokine subfamily A (Cys-Cys),
 CC member 21 (SCVA21) gene. The polynucleotide comprises polymorphic sites
 CC referred to as P51-5 to designate the order in which they are located in

CC the gene. The polymorphisms and haplotypes of SCVA21 gene are useful for
 CC validating whether SCVA21 is a suitable target for drugs to treat
 CC immunological disorders and disorders associated with its abnormal
 CC expression or function, screening for such drugs and reducing bias in
 CC clinical trials of such drugs. Haplotype information would be useful in
 CC improving the efficiency and output of several steps in the drug
 CC discovery and development process, including target validation,
 CC identifying lead compounds and early phase clinical trials. The methods
 CC are useful in screening for compounds targeting SCVA21 to treat a
 CC specific condition or disease predicted to be associated with SCVA21
 CC activity, e.g. immunological disorders. This sequence represents an
 CC allele specific oligonucleotide primer used to identify polymorphic sites
 CC in the SCVA21 gene
 XX
 SQ Sequence 15 BP; 3 A; 3 C; 4 G; 4 T; 0 U; 1 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 401 TCAGGACTGTCACGT 415
 DB 1 TCAGGACTGTCACGT 15
 RESULT 213
 AAQ96309/C
 ID AAQ96309 standard; DNA; 16 BP.
 XX
 AC AAQ96309;
 DT 28-FEB-1996 (first entry)
 XX
 DE p53 gene hybridisation probe.
 XX
 XX p53 gene; hybridisation probe; detection; tumour; cancer;
 KW Chemoprevention; chemotherapy; ss.
 OS Synthetic.
 XX
 PN WO9519448-A1.
 XX
 PD 20-JUL-1995.
 XX
 PF 13-JAN-1995; 95WO-US000657.
 XX
 PR 14-JAN-1994; 94US-00181664.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
 XX
 PI Sidransky D;
 XX
 DR WPI; 1995-263876/34.
 XX
 PT Detection of a target neoplastic nucleic acid and treatment of tumours -
 PT provides a rapid and accurate detection of mutant sequences.
 XX
 PS Example 1; Page 37; 126pp; English.
 CC
 CC AAQ96305-Q96363 are p53 gene hybridisation probes, used in the
 CC development of a new method for the detection of mutant nucleotide
 CC sequences associated with primary tumours. The method may be used to
 CC screen high risk populations, and to monitor patients undergoing
 CC chemoprevention or chemotherapy
 XX
 SQ Sequence 16 BP; 1 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 111 ATGCCGACGACGACG 125
 |||||

Db 15 ATGGCGCAGACGGG 1

RESULT 214
ABF45449
ID ABF45449 standard; DNA; 13 BP.
XX AC ABF45449;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 145446 for detecting SNP TSC0036625.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 151965; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
XX Query Match 0.8%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 95;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1415 CAACCTTCAAAAAA 1427
DB 13 CAACCTTCAAAAAA 1

RESULT 216
ABF45448/c
ID ABF45448 standard; DNA; 13 BP.
XX AC ABF45448;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 145445 for detecting SNP TSC0036625.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.

Db 249 CTCTACCGAAAAA 261
DB 1 CTCTACCGAAAAA 13

RESULT 215
ABF51968/c
ID ABF51968 standard; DNA; 13 BP.
XX AC ABF51968;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 151965 for detecting SNP TSC0038398.

XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WIPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 145445; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABT0010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 2 A; 1 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 249 CTCTACCGAAAAA 261
 DB 13 CTCTACCGAAAAA 1
 RESULT 217
 ABF51969
 ID ABF51969 standard; DNA; 13 BP.
 XX AC ABF51969;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 151966 for detecting SNP TSC0038398.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WIPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 151966; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABT0010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 8 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1415 CAACCTTCAAAAAA 1427
 DB 1 CAACCTTCAAAAAA 13
 RESULT 218
 AAT14275/C
 ID AAT14275 standard; DNA; 14 BP.
 XX AC AAT14275;
 XX DT 29-MAY-1996 (first entry)
 XX DE IL-4 and/or IL-13 activated STAT protein binding oligonucleotide.
 XX Promoter; heterologous gene; transcriptional regulatory protein; IL-4;
 XX IL-13; STAT protein; transcriptional modulation; ss.
 XX Synthetic.
 XX WO9528482-A2.
 XX PD 26-OCT-1995.
 XX PF 10-APR-1995; 95WO-US004477.
 XX PR 14-APR-1994; 94US-00228935.
 XX PR 27-MAR-1995; 95US-00410780.
 XX PA (LIGA-) LIGAND PHARM INC.
 XX PI Seidel HM, Lamb IP;
 XX WIPI; 1995-373797/48.
 XX DNA spacer regulatory elements responsive to cytokine(s) - for detecting
 XX the presence of transcriptional regulatory protein in a sample.
 XX Claim 40; Page 131; 135pp; English.
 XX The present oligonucleotide when operably linked to a promoter, and a
 CC heterologous gene (HG) selectively binds to an activated transcriptional
 CC regulatory protein, comprising a IL-4 and/or IL-13 activated STAT
 CC protein, and transcriptionally modulates the HG
 XX SQ Sequence 14 BP; 2 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 721 ACTTCCAGGAGAC 733
 DB 14 ACTTCCAGGAGAC 2

RESULT 219

AAT14274

ID AAT14274 standard; DNA; 14 BP.

XX

XX

AC

XX

XX

DT

29-MAY-1996

(first entry)

XX

XX

DE

IL-4 and/or IL-13 activated STAT protein binding oligonucleotide.

XX

XX

KW

Promoter; heterologous gene; transcriptional regulatory protein; IL-4;

XX

KW

IL-13; STAT protein; transcriptional modulation; ss.

XX

OS

Synthetic.

XX

XX

PN

WO9528482-A2.

XX

XX

PD

26-OCT-1995.

XX

XX

PF

10-APR-1995;

95WO-US004477.

XX

XX

PR

14-APR-1994;

94US-00228935.

XX

PR

27-MAR-1995;

95US-00410780.

XX

XX

PA

(LIGA-) LIGAND PHARM INC.

XX

XX

PI

Seidel HM, Lamb IP;

XX

XX

DR

WPI; 1995-373797/48.

XX

XX

PT

DNA spacer regulatory elements responsive to cytokine(s) - for detecting

XX

XX

PT

the presence of transcriptional regulatory protein in a sample.

XX

XX

PS

Claim 40; Page 131; 135pp; English.

XX

XX

CC

The present oligonucleotide when operably linked to a promoter, and a

XX

CC

heterologous gene (HG) selectively binds to an activated transcriptional

XX

CC

regulatory protein, comprising a IL-4 and/or IL-13 activated STAT

XX

CC

protein, and transcriptionally modulates the HG

XX

XX

SQ

Sequence 14 BP; 5 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match : 0.8%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 ACTTCCCGAGAAC 733

|||||

1 ACTTCCCGAGAAC 13

Db

RESULT 220

AAT41588

ID AAT41588 standard; DNA; 14 BP.

XX

XX

AC

AAT41588;

XX

XX

DT

04-JUN-1997

(first entry)

XX

XX

DE

Cytokine activated STAT6 protein dependent DNA regulatory element.

XX

XX

KW

Regulatory element; STAT6; protein; cytokine; responsive; host cell;

XX

KW

transfection; agonist; antagonist; mediated; transcription; modulation;

XX

KW

signalling pathway; ss.

XX

XX

OS

Synthetic.

XX

XX

PN

WO9630515-A1.

XX

XX

PD

03-OCT-1996.

XX

XX

PF 25-MAR-1996; 96WO-US004012.
 XX
 PR 27-MAR-1995; 95US-00411020.
 XX
 PA (LIGA-) LIGAND PHARM INC.
 XX
 PI Seidel HM, Lamb IP, Tian Chan S;
 XX
 PI WPI; 1996-455362/45.
 XX
 DR
 XX
 PT DNA construct for screening modulators of cytokine-mediated transcription
 PT - contg. regulatory element and a cytokine-sensitive promoter operably
 PT linked to a heterologous gene.
 XX
 PS Claim 15; Page 63; 72pp; English.
 XX
 CC A novel DNA construct comprises an oligonucleotide (ON) comprising a
 CC regulatory element having the present sequence, operably linked to a
 CC promoter, which is operably linked to a heterologous gene (preferably a
 CC marker gene). The gene is under the transcriptional control of the
 CC promoter and the ON sequence when the ON is bound by a STAT6 protein
 CC activated in response to IL-2, IL-3, G-CSF, GM-CSF, erythropoietin,
 CC thrombopoietin, or preferably IL-4, IL-7, IL-9, IL-13 or IL-15. Cytokine
 CC responsive host cells transfected with the DNA construct can be used to
 CC measure the ability of a compound to act as an agonist or antagonist of
 CC cytokine mediated gene transcription. In particular, they can be used to
 CC screen for cytokine modulators involved in the STAT6 protein signalling
 CC pathway
 XX
 SQ Sequence 14 BP; 5 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match : 0.8%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 ACTTCCCGAGAAC 733
 |||||
 1 ACTTCCCGAGAAC 13
 Db

RESULT 221
 AAV61625
 ID AAV61625 standard; DNA; 14 BP.
 XX
 AC AAV61625;
 XX
 XX 02-DEC-1998 (first entry)
 XX
 DE Regulatory element containing oligonucleotide #160.
 XX
 KW Cytokine-responsive regulatory; primer; promoter; detection; isolation;
 KW transcriptional control; STAT protein; screening; agonist; ss.
 XX
 OS Synthetic.
 XX
 XX US5814517-A.
 XX
 XX 29-SEP-1998.
 XX
 PF 27-MAR-1995; 95US-00410779.
 XX
 PR 14-APR-1994; 94US-00228935.
 XX
 PA (LIGA-) LIGAND PHARM INC.
 XX
 PI Lamb IP, Seidel HM;
 XX
 PI WPI; 1998-541763/46.
 XX
 XX DNA constructs containing cytokine-responsive regulatory elements -
 PT useful in assays for transcription-regulating proteins or gene
 PT transcription agonists or antagonists.
 XX

PS Example 3; Col 33-34; 58pp; English.

XX AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
 CC production of constructs comprising a cytokine-responsive regulatory
 CC element linked to a promoter which is linked to a heterologous coding
 CC sequence so that the coding sequence is under the transcriptional control
 CC of the regulatory element and the promoter, where the regulatory element
 CC has a nucleotide sequence selected from TTGNGGAA, TTANYTAA, and TTCNYTAA
 CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to
 CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,
 CC in a sample by contacting the sample with the construct so that the
 CC protein binds to the regulatory element, and detecting or separating the
 CC resulting complex. The cells can be used in screening assays for agonists
 CC of gene transcription, in which the level of expression of the coding
 CC sequence is measured in the presence and absence of a test compound or in
 CC the presence of the corresponding cytokine

XX Sequence 14 BP; 5 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 ACTTCCAGGAC 733
 Db 1 ACTTCCAGGAC 13

RESULT 222
 ID AAV61626/C
 AC AAV61626 standard; DNA; 14 BP.

XX AAV61626;
 XX 02-DEC-1998 (first entry)
 XX Regulatory element containing oligonucleotide #161.

XX Cytokine-responsive regulatory; primer; promoter; detection; isolation;
 XX transcriptional control; STAT protein; screening; agonist; ss.

XX Synthetic.
 XX US5814517-A.

XX 29-SEP-1998.
 XX 27-MAR-1995; 95US-00410779.
 XX 14-APR-1994; 94US-00228935.

XX (LIGA-) LIGAND PHARM INC.

XX Lamb 1P, Seidel HM;

XX WPI; 1998-541763/46.

XX DNA constructs containing cytokine-responsive regulatory elements -
 XX useful in assays for transcription-regulating proteins or gene
 XX transcription agonists or antagonists.

PS Example 3; Col 33-34; 58pp; English.

XX AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
 CC production of constructs comprising a cytokine-responsive regulatory
 CC element linked to a promoter which is linked to a heterologous coding
 CC sequence so that the coding sequence is under the transcriptional control
 CC of the regulatory element and the promoter, where the regulatory element
 CC has a nucleotide sequence selected from TTGNGGAA, TTANYTAA, and TTCNYTAA
 CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to
 CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,
 CC in a sample by contacting the sample with the construct so that the
 CC protein binds to the regulatory element, and detecting or separating the

CC resulting complex. The cells can be used in screening assays for agonists
 CC of gene transcription, in which the level of expression of the coding
 CC sequence is measured in the presence and absence of a test compound or in
 CC the presence of the corresponding cytokine

XX Sequence 14 BP; 2 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 721 ACTTCCAGGAC 733
 Db 14 ACTTCCAGGAC 2

RESULT 223
 ID AAQ51221
 AC AAQ51221 standard; DNA; 15 BP.

XX AAQ51221;
 XX 25-MAR-2003 (revised)
 XX 12-APR-1994 (first entry)

XX Vaccinia regulatory element sequence.

XX Inhibition; viral replication; infection; ss.

XX Synthetic.

XX WO9320694-A1.

XX 28-OCT-1993.

XX 14-APR-1993; 93WO-US003567.

XX 14-APR-1992; 92US-00868539.

XX (SIGN-) SIGNAL PHARM INC.

XX Carman MD;

XX WPI; 1993-351240/44.

XX Viral replication inhibition in infected cell for e.g. herpes simplex
 XX virus-1 - by selecting deoxyribonucleic acid fragment, contg. covalently
 XX linked strands with sequence corresp. to regulatory element in virus, and
 XX introducing in cell.

XX Disclosure; Fig 4; 28pp; English.

XX The viral regulatory sequence from Vaccinia may be introduced into cells
 XX to inhibit replication of the virus in the cell and to inhibit viral
 XX infection. See also AAQ51213-20. (Updated on 25-MAR-2003 to correct PN
 XX field.)

XX Sequence 15 BP; 9 A; 1 C; 1 G; 3 T; 0 U; 1 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 1.2e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 257 AAAAATGGAATCTA 271
 Db 1 AAAAATGGAATCTA 15

RESULT 224
 ID AAT55111
 AC AAT55111 standard; RNA; 15 BP.

XX AAT55111;

XX	25-MAR-2003	(revised)	Human relA hammerhead ribozyme target sequence (nt. position 996).
DT	21-APR-1997	(first entry)	
XX			Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX			gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW			intercellular adhesion molecule; rel A; tumour necrosis factor;
KW			TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW			translocation; chronic myelogenous leukaemia; CML; cancer;
KW			Philadelphia chromosome; inflammation; autoimmune disease;
KW			atherosclerosis; myocardial infarction; stroke; restenosis;
KW			transplant rejection; rheumatoid arthritis; psoriasis;
KW			myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW			human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX			ss.
OS			Homo sapiens.
XX			WO9523225-A2.
PN			31-AUG-1995.
XX			23-FEB-1995;
PF			95WO-IB000156.
XX			23-FEB-1994;
PR			94US-00201109.
PR			29-MAR-1994;
PR			94US-00218934.
PR			04-APR-1994;
PR			94US-00222795.
PR			07-APR-1994;
PR			94US-00224483.
PR			15-APR-1994;
PR			94US-00227958.
PR			15-APR-1994;
PR			94US-00228041.
PR			18-MAY-1994;
PR			94US-00245736.
PR			06-JUL-1994;
PR			94US-00271280.
PR			15-AUG-1994;
PR			94US-00291932.
PR			16-AUG-1994;
PR			94US-00291433.
PR			17-AUG-1994;
PR			94US-00292620.
PR			19-AUG-1994;
PR			94US-00293520.
PR			02-SEP-1994;
PR			94US-00300000.
PR			08-SEP-1994;
PR			94US-00303039.
PR			23-SEP-1994;
PR			94US-00311486.
PR			23-SEP-1994;
PR			94US-00311749.
PR			28-SEP-1994;
PR			94US-00314397.
PR			03-OCT-1994;
PR			94US-00316771.
PR			07-OCT-1994;
PR			94US-00319492.
PR			11-OCT-1994;
PR			94US-00321993.
PR			04-NOV-1994;
PR			94US-00334847.
PR			10-NOV-1994;
PR			94US-00337608.
PR			28-NOV-1994;
PR			94US-00345516.
PR			16-DEC-1994;
PR			94US-00357577.
PR			23-DEC-1994;
PR			94US-00363233.
PR			30-JAN-1995;
PR			95US-00380734.
XX			(RIBO-) RIBOZYME PHARM INC.
XX			Stinchcomb DT, Chowira B, Drenzo A, Draper KG, Dudycz LW;
PI			Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI			Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI			Tracz D, Usman N, Wincott FE, Woolf T;
XX			WPI; 1995-351090/45.
DR			Ribozymes having modified bases and methods for producing them - for use
XX			in inhibiting disease related genes.
PT			Claim 2; Page 229; 407pp; English.
XX			The present sequence represents a preferred target sequence for an
CC			enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
CC			nucleotide base position indicated in the DE line. The relA gene product
CC			is a subunit of the transcriptional regulator NF-kappaB and is implicated
CC			specifically in the induction of inflammatory responses. Regions of the
CC			mRNA that do not form secondary folding structures and that contain

CC	potential hammerhead and hairpin ribozyme cleavage sites were identified
CC	by computer analysis. Ribozymes directed against these mRNA sequences
CC	were designed and synthesised with modifications that improve their
CC	nuclease resistance. The ribozymes are designed to cleave the target
CC	sequences and thereby inhibit relA expression, making them potentially
CC	useful for treating rheumatoid arthritis, restenosis and asthma as well
CC	as for increasing tolerance to transplanted tissues. The potential
CC	immunosuppressive properties of a ribozyme that cleaves relA mRNA means
CC	that uses are limited to local delivery, acute indications or ex vivo
CC	treatment. (Updated on 25-MAR-2003 to correct PI field.)
XX	Sequence 15 BP; 6 A; 3 C; 4 G; 0 T; 2 U; 0 Other;
SQ	Query Match 0.8%; Score 13; DB 1; Length 15;
	Best Local Similarity 84.6%; Pred. No. 1.2e+02;
	Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY	1045 GGACATATGAGAC 1057
DB	2 GGACAUAGAGAC 14
RESULT 225	
AAT49860	
ID	AAT49860 standard; RNA; 15 BP.
AC	AAT49860;
XX	
DT	07-MAR-1997 (first entry)
XX	
DE	Human CERP HH ribozyme target sequence #1542.
XX	
KW	Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW	neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW	reverse cholesterol transport; high density lipoprotein; therapy; CERP;
KW	familial hypercholesterolaemia; dyslipidaemia; hypocalphaipoproteinaemia;
KW	peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW	angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW	LDL; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9620279-A1.
XX	
PD	04-JUL-1996.
XX	
PF	11-DEC-1995; 95WO-US016000.
XX	
PR	23-DEC-1994; 94US-00363240.
XX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(WARN) WARNER LAMBERT CO.
XX	
PI	Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Page M;
XX	
DR	WPI; 1996-321852/32.
XX	
PT	New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
PT	useful for preventing or treating initial development, progression or
PT	regression of vascular diseases, esp. familial hypercholesterolaemia.
XX	
PS	Claim 4; Page 33; 72pp; English.
XX	
CC	AAT49608-T49863 represent target sequences for the human cholesterol
CC	ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT49881-
CC	T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid
CC	transfer between plasma lipoproteins. The numbering of the targets refers
CC	to the position of the cleavage site in full length CERP. The ribozyme
CC	binds to 5 nucleotides either side of this site, provided the sequence
CC	is immediately upstream. The ribozymes are able to cleave mRNA from the
CC	gene encoding CERP, thereby blocking synthesis and/or expression of the
CC	mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway
CC	can be inhibited (or eliminated) thereby preventing the reduction in size

CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CERP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetaloproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CERP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CERP mRNA. As the HH
CC ribozymes target specific regions of the CERP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 1 A; 4 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1577 TGGCTTCCTGCTG 1589
Db 3 UGGCUUCUGCUG 15

RESULT 226
AAT49861
ID AAT49861 standard; RNA; 15 BP.
AC AAT49861
XX
DT 07-MAR-1997 (first entry)
XX
DE Human CERP HH ribozyme target sequence #1543.

XX Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KW reverse cholesterol transport; high density lipoprotein; therapy; CERP.
KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
KW LDL; ss.
XX
OS Homo sapiens.
XX
XX WO9620279-A1.
XX
XX 04-JUL-1996.
XX
XX 11-DEC-1995; 95WO-US016000.
XX
XX 23-DEC-1994; 94US-00363240.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (WARN) WARNER LAMBERT CO.
XX
XX Couture L, Stinchcomb D, Meswigen J, Bisgaier C, Page M;
XX WPI; 1996-321862/32.
XX

XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
XX useful for preventing or treating initial development, progression or
XX regression of vascular diseases, esp. familial hypercholesterolaemia.
XX
XX Claim 4; Page 33; 72pp; English.
XX
XX AAT49608-T49863 represent target sequences for the human cholesterol
XX ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT4981-
XX T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid
XX transfer between plasma lipoproteins. The numbering of the targets refers
XX to the position of the cleavage site in full length CERP. The ribozyme
XX binds to 5 nucleotides either side of this site, provided the sequence UH
XX is immediately upstream. The ribozymes are able to cleave mRNA from the

CC gene encoding CERP, thereby blocking synthesis and/or expression of the
CC mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway
CC can be inhibited (or eliminated) thereby preventing the reduction in size
CC density of the high density lipoproteins (HDL), prolonging HDL half life,
CC and therefore increasing HDL levels. The ribozymes can be used to treat
CC conditions associated with abnormal levels of CERP, specifically familial
CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
CC hyperbetaloproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
CC vascular complications of diabetes, transplant, atherectomy and
CC angioplastic restenosis. By inhibiting CERP, the levels of HDL and low
CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
CC The HH ribozymes can also be used diagnostically to study genetic drift
CC and mutations in diseased cells, and to detect CERP mRNA. As the HH
CC ribozymes target specific regions of the CERP gene, they have low non-
CC specific activity
XX
SQ Sequence 15 BP; 1 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1577 TGGCTTCCTGCTG 1589
Db 2 UGGCUUCUGCUG 14

RESULT 227
AAV28329/C
ID AAV28329 standard; DNA; 15 BP.
XX
AC AAV28329;
XX
DT 12-OCT-1998 (first entry)
XX
DE DNA EDTA probe (7) fragment.

XX ss; probe; EDTA probe; specific sequence recognition;
KW chemotherapeutic agent; homopyrimidine-homopurine tract.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 22 /*tag= a
XX /note= "EDTA thymidine"
XX
XX US5789155-A.
XX
XX 04-AUG-1998.
XX
XX 12-NOV-1993; 93US-00152250.
XX
XX 30-OCT-1987; 87US-00115922.
XX 16-NOV-1990; 90US-00614205.
XX
XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Moser HE, Dervan PB;
XX WPI; 1998-446067/38.
XX
XX Detection of double-stranded nucleic acid sequence - with triplex-forming
XX oligonucleotide probe.
XX
XX Example 2; Fig 4B; 18pp; English.

XX The EDTA probes 1-9 shown in sequences AAV28326-V28330 contain a single
XX thymidine with EDTA covalently attached at C-5. The probes are used for
XX specific recognition and cleavage of double-stranded DNA or RNA at a
XX sequence specific loci using a triple helix intermediary. The method
XX allows the delivery of chemotherapeutic agents in vivo an eliminates the

CC need to denature the DNA before the agent can act. The method allows
CC precise location of a chemotherapeutic agent or replacement gene sequence
CC at a specific homopyrimidine-homopurine tract anywhere in a large double-
CC stranded nucleic acid. This method allows diagnosis of gene based
CC diseases, and eliminates the need for many steps in the commonly used
CC diagnostic processes
XX

SQ Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1453 AAAAAGAGAAGA 1465
DB 15 AAAAAGAGAAGA 3

RESULT 228
AAV48734/C
ID AAV48734 standard; DNA; 15 BP.

XX AC AAV48734;
XX AC AAV48734;
XX 15-OCT-1998 (first entry)
XX Erbb-2 gene antisense oligonucleotide Erbb-2-26.
XX Erbb-2; antisense oligonucleotide; modulate; gene expression; ss.

XX Synthetic.
XX Homo sapiens.
XX EP856579-A1.
XX 05-AUG-1998.
XX 31-JAN-1997; 97EP-00101531.
XX 31-JAN-1997; 97EP-00101531.
XX (BIOG-) BIOGNOSTIK GBS BIOMOLEKULARE DIAGNOSTIK.
XX Schlingensiepen K, Brysch W;
XX WPI; 1998-400910/35.

XX Preparation of antisense oligonucleotide(s) which lack long runs of
XX consecutive guanosine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX Claim 10; Fig 6a; 286pp; English.

XX AAV48709-886 represent antisense oligonucleotides directed against the
XX Erbb-2 gene. Of these, only oligonucleotides AAV48709-91 resulted in
XX significant reduction in Erbb-2 protein expression, while
XX oligonucleotides AAV48792-886 had little effect. The oligonucleotides
XX exemplify the invention. The specification describes oligonucleotides
XX that contain 8-30 nucleotides, which contain at most 8 nucleotides that
XX can each form three hydrogen bonds to cytosine; do not contain four
XX consecutive nucleotides able to form three H-bonds each to four
XX consecutive cytosines; do not contain two sequences of three consecutive
XX nucleotides each able to form three H-bonds to three consecutive
XX cytosines, and the ratio between residues able to form two H-bonds each
XX (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
XX oligonucleotides are used to modulate expression of genes, particularly
XX the genes for p53, Erbb-2, junB, jund, TGF-beta 1 or beta 2 to control
XX proliferation of primary cell cultures (e.g. bone marrow stem, liver or
XX kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
XX oligonucleotides can also be used to analyse function of proteins (by
XX altering their expression or activity) and therapeutically, e.g. in cases

CC of cancer or (targeting TGF) for stimulating the immune system
XX
SQ Sequence 15 BP; 2 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1377 TCTGAAGAGGAGG 1389
DB 13 TCTGAAGAGGAGG 1

RESULT 229
AAX31318
ID AAX31318 standard; DNA; 15 BP.

XX AAX31318;
XX 21-MAY-1999 (first entry)
XX Tag sequence of a transcript decreased in colorectal cancer.
XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;
XX diagnosis; prognosis; treatment; ss.

XX Homo sapiens.
XX WO9853319-A2.
XX 26-NOV-1998.
XX 20-MAY-1998; 98WO-US010277.
XX 21-MAY-1997; 97US-0047352P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Vogelstein B, Kinzler KW;
XX WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products for the
XX diagnosis, prognosis and treatment of cancers, particularly colon and
XX pancreatic cancer.

XX Claim 1; Page 43; 120pp; English.
XX AAX30947-31815 represent tag sequences of transcripts that are
XX differentially expressed in colorectal cancer, in pancreatic cancer, or
XX in both. The tag sequences can be used to identify genes by matching the
XX tag to a Gen data base member, or by using the tag sequences as probes to
XX isolate unidentified genes from cDNA libraries. The tag sequences can
XX also be used in a method for diagnosing colon or pancreatic cancer in a
XX sample suspected of being neoplastic. The method comprises comparing the
XX level of at least one transcript in a first sample of a tissue to a
XX second sample, where the first sample is a colonic tissue suspected of
XX being neoplastic and the second sample is a normal human colonic tissue.
XX The transcript is identified by a tag selected from AAX30947-31815. The
XX methods of the invention can be used in the diagnosis, prognosis and
XX treatment of cancer

SQ Sequence 15 BP; 1 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 513 TGGGCTGGGGGCC 525
DB 3 TGGGCTGGGGGCC 15

```

RESULT 230
AAFS3138
ID AAF53138 standard; DNA; 15 BP.
XX
XX AAF53138;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #4098.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO2000078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 8; Page 87; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 5 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1397 GGGCGCGCAAGAAC 1409
XX
XX 1 GGGCGCGCAAGAAC 13
XX
XX
XX
XX RESULT 231
AAAF48239/C
ID AAF48239 standard; DNA; 15 BP.
XX
XX

```

```

AC AAF48239;
XX
XX 30-MAR-2001 (first entry)
XX
XX IGFBP3 oligonucleotide #1659.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
XX
XX WO2000078341-A1.
XX
XX 28-DEC-2000.
XX
XX 21-JUN-2000; 2000WO-AU000693.
XX
XX 21-JUN-1999; 99US-0140345P.
XX
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.
XX
XX Example 7; Page 55; 201pp; English.
XX
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX
XX Sequence 15 BP; 1 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1378 CTCAGAGGAGGG 1390
XX
XX 15 CTCAGAGGAGGG 3
XX
XX
XX
XX RESULT 232
AAAF48240/C
ID AAF48240 standard; DNA; 15 BP.
XX
XX AAF48240;
XX
XX 30-MAR-2001 (first entry)
XX
XX

```

DE IGFBP3 oligonucleotide #1660.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;

KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;

KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;

KW hyperneovascular condition; hyperplasia; kidney disease;

XX neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

PN 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

PF 21-JUN-1999; 99US-0140345P.

PR (MURD-) MURDOCH CHILDRENS RES INST.

XX Wright CJ, Werther GA, Edmondson SR;

PI WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering

PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that

PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.

XX Example 7; Page 55; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an

CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1

CC receptor, IGF binding protein [IGBP]-2 or IGFBP3), which is capable of

CC inhibiting or reducing growth factor mediated cell proliferation,

CC inflammation and/or other disorders. The present sequence is an

CC oligonucleotide which can be used to design the antisense

CC oligonucleotides of the present invention (see AAF45151 and AAF45153-

CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,

CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,

CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia

XX

SQ Sequence 15 BP; 1 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1378 CTGACGAGGAGGG 1390

DB 14 CTGACGAGGAGGG 2

RESULT 233

ID ABK95779

XX ABK95779 standard; DNA; 15 BP.

XX AC ABK95779;

XX 24-SEP-2002 (first entry)

DT

XX Solute Carrier Family 1 (SLC1A4) allele-specific oligonucleotide #19.

DE

XX Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;

KW glutamate/neutral amino acid transporter; neurological disease; PCR; ss;

KW

KW amino acid transporter disorder; single nucleotide polymorphism; SNP.

XX Homo sapiens.

XX WO200244198-A2.

XX 06-JUN-2002.

XX 29-NOV-2001; 2001WO-US044781.

XX 30-NOV-2000; 2000US-0250254P.

XX (GENA-) GENAISANCE PHARM INC.

XX Bieglecki KM, Kazemi A, Russo DP, Sausker EA;

XX WPI; 2002-519580/55.

XX Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral

PT Amino Acid transporter), Member 4 isoenzymes, for improving efficiency and

PT reliability in drug development for treating cancers.

XX Claim 15; Page 15; 139pp; English.

XX The invention relates to an isolated polynucleotide (I) comprising a

CC first nucleotide sequence which comprises solute carrier family 1

CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isoenzymes

CC (II) and an isolated polypeptide (III) comprising an amino acid sequence

CC which is a polymorphic variant of a reference sequence for SLC1A4

CC protein. Also described are methods for: (1) haplotyping or genotyping

CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4

CC gene of an individual; (3) identifying an association between a trait and

CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) Is useful

CC in screening for drugs targeting (III) that are useful for treating

CC cancer, neurological diseases and amino acid transporter disorders. The

CC methods are useful for improving the efficiency and reliability of

CC several steps in the discovery and development of drugs for treating

CC diseases associated with SLC1A4 activity. The haplotyping method is also

CC used by the pharmaceutical research scientist to validate SLC1A4 as a

CC candidate target for treating a specific condition or disease predicted

CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases

CC and amino acid transporter disorders, and in the design of clinical

CC trials for treating a specific condition of disease associated with

CC SLC1A4 activity. The methods are also useful for screening compounds

CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,

CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4

CC gene allele-specific oligonucleotides, primer extension oligonucleotides

CC and related PCR primers used to identify single nucleotide polymorphisms

CC (SNP) of the gene

XX

SQ Sequence 15 BP; 2 A; 5 C; 5 G; 2 T; 0 U; 1 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 1.2e+02;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 522 GGCTGACCATGCA 536

DB 1 GGCTGACCATGCA 15

RESULT 234

ID ABQ88675/c

XX ABQ88675 standard; DNA; 15 BP.

XX AC ABQ88675;

XX 23-SEP-2002 (first entry)

DT

XX Human CFL1 ASO PCR primer #22.

DE

XX Human; cofilin 1; CFL1; gene therapy; antisense gene therapy; primer;

KW immunological disorder; ASO; allele-specific oligonucleotide; PCR; ss.

KW

XX OS Homo sapiens.
 XX PN WO200194376-A1.
 XX PD 13-DEC-2001.
 XX PF 11-JUN-2001; 2001WO-US018815.
 XX PR 09-JUN-2000; 2000US-0210884P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Anaetasio AB, Duda A, Klien SE, Koshy B, Sausker EA;
 XX DR WPI; 2002-566437/60.
 XX PT Novel genetic variants of human cofilin 1, CFL1 gene for studying
 PT expression, function of the gene and expressing CFL1 protein useful in
 PT identifying drugs to treat immunological disorders.
 XX PS Claim 17; Page 13; 84pp; English.
 XX CC The invention relates to a novel polynucleotide sequence which is a
 CC polymorphic variant of a reference sequence for the cofilin 1 (non-
 CC muscle) (CFL1) gene or its fragment, or a polymorphic variant of a
 CC reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of
 CC the invention may have a use in gene therapy, and in antisense gene
 CC therapy. The polynucleotide is useful for studying the expression and
 CC function of CFL1 and expressing CFL1 protein for use in screening for
 CC candidate drugs to treat diseases related to CFL1 activity. The
 CC polymorphism and haplotype data are useful for validating whether CFL1 is
 CC a suitable target for drugs to treat immunological disorders, screening
 CC for such drugs and reducing bias in clinical trials of such drugs. The
 CC present sequence represents one of a set of allele-specific
 CC oligonucleotide (ASO) PCR primer used in the invention to detect
 CC polymorphisms in the CFL1 gene
 XX SQ Sequence 15 BP; 5 A; 6 C; 2 G; 1 T; 0 U; 1 Other;
 Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 1.2e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 994 TGCTGATGCTGGGAG 1008
 Db :|||||
 15 TRCTGTGCTGGGAG 1
 RESULT 235
 ABT05320/c
 ID ABT05320 standard; DNA; 15 BP.
 AC ABT05320;
 XX 24-OCT-2002 (first entry)
 DT Human N-acetylgalactosaminidase (NAGA) alpha gene ASO primer 12.
 DE Human; PCR; primer; ss; gene therapy; N-acetylgalactosaminidase alpha;
 XX chromosome 22q13.2-q13.31; lysosomal glycosidase; screening; SNP;
 KW NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
 KW genotyping.
 XX OS Homo sapiens.
 XX PN WO200194637-A1.
 XX PD 13-DEC-2001.
 XX PF 07-JUN-2001; 2001WO-US018456.
 XX PR 07-JUN-2000; 2000US-0210110P.

XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Duda A, Kazemi A, Koshy B, Parks KE;
 XX DR WPI; 2002-566449/60.
 XX PT New genetic variants of isolated N-acetylgalactosaminidase (NAGA), Alpha
 PT gene, useful for therapeutic purposes, for studying the expression and
 PT function of the polynucleotide, and for expressing NAGA protein.
 XX PS Claim 16; Page 13; 91pp; English.
 XX CC The invention comprises the amino acid and coding sequence of the human N
 CC -acetylgalactosaminidase (NAGA) alpha protein. The invention specifically
 CC comprises novel polymorphic sites identified within the NAGA gene. The
 CC NAGA gene is located on chromosome 22q13.2-q13.31, and encodes a
 CC lysosomal glycosidase that cleaves alpha-N-acetylgalactosaminyl
 CC moieties in glycoconjugates. The NAGA DNA and protein sequences of the
 CC invention are useful for studying the expression and function of NAGA and
 CC for screening candidate drugs to treat diseases related to NAGA activity.
 CC The NAGA gene polymorphisms identified in the present invention are
 CC useful for haplotyping and genotyping the NAGA gene of an individual. The
 CC present DNA sequence represents an N-acetylgalactosaminidase gene allele-
 CC specific oligonucleotide primer
 XX SQ Sequence 15 BP; 4 A; 2 C; 3 G; 5 T; 0 U; 1 Other;
 Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 1.2e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 633 ATTGATATTCACCAT 647
 Db :|||||
 15 AYTGATAGTCACCAT 1
 RESULT 236
 ABQ83689/c
 ID ABQ83689 standard; DNA; 15 BP.
 AC ABQ83689;
 XX 27-JAN-2003 (first entry)
 DT DNA-templated synthesis related oligonucleotide #48.
 DE Molecular function; diversification; selection; amplification; evolve;
 XX synthesis; library; chemical compound; hybridisation; ss.
 KW Synthetic.
 XX OS WO200274929-A2.
 XX PN 26-SEP-2002.
 XX PD 19-MAR-2002; 2002WO-US008546.
 XX PF 19-MAR-2001; 2001US-0277081P.
 XX PR 19-MAR-2001; 2001US-0277094P.
 XX PR 20-JUL-2001; 2001US-0306691P.
 XX PR 19-MAR-2002; 2002US-00101030.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Liu DR, Gartner ZJ, Kanan MW;
 XX DR WPI; 2002-740858/80.
 XX PT Synthesizing chemical compounds by hybridizing one or more templates
 PT which have associated reactive unit, with one or more transfer units
 PT having anti-codon and reactive unit, and performing reaction of reactive
 PT units.

XX PS Example 7; Fig 44; 146pp; English.

CC The present invention describes a method (M1) for synthesising one or more chemical compounds. M1 involves providing one or more templates, which optionally have a reactive unit associated with them; and contacting one or more transfer units having an anti-codon and reactive unit with the one or more templates under conditions to allow for hybridisation of the one or more anti-codons to template, and reaction of the reactive units. Also described: (1) a method (M2) of evolving a library of compounds; (2) a kit comprising one or more nucleic acid templates and one or more transfer units; (3) a method (M3) for synthesising one or more non-natural polymers; and (4) a library (L) comprising one or more chemical compounds where each of the chemical compounds is bonded to an amplifiable template whose nucleotide sequence is informative of the structure of the chemical compounds, where the library is synthesised by M1 or M3. The method can be used for synthesising one or more chemical compounds which contain an anti-codon comprising a nucleotide sequence which hybridises with one or more nucleic acid templates. M1 is useful for synthesising a library of chemical compounds. The methods are useful for synthesising chemical compounds that are not, or do not resemble nucleic acids or nucleic acid analogues. The present sequence represents an oligonucleotide which is used in an example from the present invention

XX SQ Sequence 15 BP; 4 A; 6 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 CCGTGGTGGTGGT 31
Db 15 CCGTGGTGGTGGT 3

RESULT 237
ABK96592

XX ID ABK96592 standard; DNA; 15 BP.

XX AC ABK96592;

XX 24-SEP-2002 (first entry)

XX Human interleukin 6 allele specific primer #15.

XX Homo sapiens.

XX WO200238586-A2.

XX 16-MAY-2002.

XX 09-NOV-2001; 2001WO-US047077.

XX 09-NOV-2000; 2000US-0247578P.

XX 21-AUG-2001; 2001US-0313963P.

XX (GENA-) GENAISANCE PHARM INC.

XX Bentivegna SC, Bieglecki KM, Chew A, Denton RR, Lachowicz M;
PI Nandabalan K, Parks KE, Sausker EA;

XX WPI; 2002-519290/55.

XX Genetic variants of interleukin-6 isogenes for improving efficiency and
PT reliability in drug development for treating myeloma, coronary artery

PT disease, arthritis and Kaposi sarcoma.

XX Claim 15; Page 15; 86pp; English.

XX The invention relates to a polynucleotide comprising a first nucleotide sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine) isogene selected from isogenes 1-11 and 13-18 given in the specification, where each isogene comprises the regions of NS1 and is further defined by the corresponding sequence of polymorphisms whose locations and identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17), or a second nucleotide sequence (NS2) complementary to NS1.

CC Alternatively, the sequence comprises a coding sequence for an IL6 isogene. Also included are methods of haplotyping/ genotyping (and predicting the haplotype/genotype) of the IL6 gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair in the IL6 gene, a recombinant non-human organism (III) a polymorphic in the IL6 gene, an isolated oligonucleotide for detecting a fragment of the IL6 isogene comprising at least 10 and containing one of the identified single- nucleotide polymorphisms (SNP), an isolated polypeptide (or fragment) comprising an amino acid sequence which is a polymorphic variant of IL6, an isolated monoclonal antibody specific for IL6, a computer system for storing and analysing polymorphism data for the IL6 gene, and a genome anthology for the IL6 gene. The IL6 gene is useful for treating myeloma, coronary artery disease (CAD), infection, HIV, hypercalcaemia, bone disease, inflammatory disease, stunted growth and systemic onset juvenile chronic arthritis. The methods are useful for improving the efficiency and reliability in the discovery of the IL6 isogene is useful in diagnostic, prognostic and therapeutic methods. The IL6 isogene is useful in studying the expression and function of IL6, and in expressing IL6 protein for use in screening for candidate drugs.

CC The gene for IL6 is located on chromosome 7p21-p15. The present sequence is an allele specific primer for an IL6 polymorphism

XX SQ Sequence 15 BP; 5 A; 2 C; 5 G; 2 T; 0 U; 1 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.2e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1537 AGGAGGAGGCGCAAGT 1551
Db 1 ATGAGGAGGCGCAAT 15

RESULT 238
ABZ34008/C

ID ABZ34008 standard; DNA; 15 BP.

XX AC ABZ34008;

XX 31-JAN-2003 (first entry)

XX HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:250.

XX Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme; detection; mutation; anti-HIV drug resistance; polymorphism; resistance; probe; ss.

XX Human immunodeficiency virus 1.

XX Synthetic.

XX WO200255741-A2.

XX 18-JUL-2002.

XX 09-JAN-2002; 2002WO-EP000153.

XX 11-JAN-2001; 2001EP-00870005.

XX 20-APR-2001; 2001EP-00870085.

PR 24-APR-2001; 2001US-0286102P.
XX (INNO-) INNOGENETICS NV.
XX De Smet K., Stuyver L;
XX WPI; 2002-590580/53.
XX
XX Detecting mutations associated with anti-HIV drug resistance comprises
PT detecting at least one of the mutations in the HIV reverse transcriptase
PT gene by using probes optimized to function together in a reverse-
PT hybridization assay.
XX
XX Claim 2; Page 19; 117pp; English.
XX
XX The present invention describes a method for detecting mutations
CC associated with anti-HIV drug resistance in a patient by detecting at
CC least one of the mutations K103N/R, Y106A/I/L, Y181C/I, M184V/I, Y188L,
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
CC of HIV strains in a biological sample using a specific set of probes
CC optimised to function together in a reverse-hybridisation assay. The
CC method and the nucleic acid sequences used in the method are useful for
CC determining viral mutations and/or polymorphisms in the HIV RT gene
CC associated with resistance. The probes are useful for the genetic
CC detection, preferably in vitro detection of the mutations K103N/R,
CC Y106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
CC mutation is associated with anti-HIV drug resistance. The method provides
CC a rapid, reliable and precise assay or determination and monitoring of
CC antiviral drug resistance or mutations associated with drug resistance of
CC viruses containing RT genes. AB233759 to AB234642 represent HIV RT
CC sequences and probes which are used in the exemplification of the present
CC invention
XX
XX Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1273 CCATCCCTGAGGA 1285
DB 15 CCATCCCTGAGGA 3
RESULT 239
ABK32272
ID ABK32272 standard; DNA; 15 BP.
XX
XX AC ABK32272;
XX
XX DT 23-APR-2002 (first entry)
XX
XX DE Human colon cancer SAGE tag #373.
XX
XX KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KW serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.
XX
XX OS Homo sapiens
XX
XX PN US6333152-B1
XX
XX PD 25-DEC-2001.
XX
XX PF 20-MAY-1998; 98US-00081646.
XX
XX PR 20-MAY-1998; 98US-00081646.
XX
XX PA (UJJO) UNIV JOHNS HOPKINS.
XX
XX FI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX

DR WPI; 2002-153821/20.
XX
XX New human nucleic acid containing specific SAGE tags, useful as
PT diagnostic markers for cancer, also derived probes.
XX
XX PS Disclosure; Col 42; 161pp; English.
XX
XX CC The invention relates to an isolated, purified human nucleic acid (I)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention
XX
XX SQ Sequence 15 BP; 1 A; 4 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 513 TGGGCTGGGGGCC 525
DB 3 TGGGCTGGGGGCC 15
RESULT 240
ABI99094
ID ABI99094 standard; DNA; 15 BP.
XX
XX AC ABI99094;
XX
XX DT 27-FEB-2002 (first entry)
XX
XX DE Human PCDH2 ASO PCR primer SEQ ID NO 51.
XX
XX KW Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;
KW single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;
KW allele-specific oligonucleotide; ASO; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200194361-A2.
XX
XX PD 13-DEC-2001.
XX
XX PF 06-JUN-2001; 2001WO-US018321.
XX
XX PR 06-JUN-2000; 2000US-0209564P.
XX
XX PA (GENA-) GENAISSANCE PHARM INC.
XX
XX PI Kliehm SE, Koshiy B, Tanguay DA;
XX
XX WPI; 2002-097928/13.
XX
XX PT New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,
PT useful in expressing PCDH2 protein for screening candidate drugs to treat
PT diseases related to PCDH2 activity.
XX
XX PS Claim 16; Page 14; 127pp; English.
XX
XX CC The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,
CC comprising determining which of the haplotypes given in the specification
CC defines one or both copies of the individual's PCDH2 gene. The
CC polymorphisms are within a 30244 base pair sequence (ABA05413), fully
CC defined in the specification. The polymorphic variants are useful in
CC studying the expression and function of PCDH2, in expressing PCDH2
CC protein for use in screening for candidate drugs to treat diseases such
CC as cancer, related to PCDH2 activity, in studying the effect of the
CC variation on the biological activity of PCDH2 and the binding affinity of
CC candidate drugs targeting PCDH2. The haplotyping methods are useful in
CC validating PCDH2 as a candidate target for treating a specific condition
CC

CC or disease predicted to be associated with PCDH2 activity or in the
 CC design of clinical trials of candidate drugs for treating a specific
 CC condition or disease associated with PCDH2 activity. The present sequence
 CC is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of
 CC the invention.

XX SQ Sequence 15 BP; 1 A; 5 C; 5 G; 3 T; 0 U; 1 Other;

Query Match 0.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGCCCGCTGGTGGTGG 29
 DB 1 TACCGCTGGTGGTGG 15

RESULT 241
 AAQ40937/C
 ID AAQ40937 standard; DNA; 16 BP.

XX AC AAQ40937;
 XX 25-MAR-2003 (revised)
 DT 08-SEP-1993 (first entry)

XX Sense running start primer to study AZT incorporation into DNA.

XX DNA polymerase; alpha catalytic polypeptide; hybridisation; ss;
 KW template-dependent enzymatic nucleic acid synthesis; screening.

XX Synthetic.

XX WO9310139-A1.

XX 27-MAY-1993.

XX 12-NOV-1992; 92WO-US009457.

XX 15-NOV-1991; 91US-00792600.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Copeland WC, Wang TSF;

XX WPI; 1993-182482/22.

XX Purified nucleic acid for enzymatic synthesis of nucleic acid - encodes
 PT human polymerase alpha catalytic polypeptide, and is contained in
 PT baculovirus vector for enhanced prodn. in insect cells.

XX Disclosure; Page 48; 84pp; English.

XX Recombinant human DNA polymerase alpha was purified from Sf9 cells
 CC infected with the AchPP alpha recombinant baculovirus and the purified
 CC enzyme used to test the incorporation of AZT into DNA. Running start and
 CC standing start primers were separately 5' end labelled with radioactive
 CC phosphate and annealed to their respective templates. Primer extension
 CC was performed and AZT was found to be incorporated into the DNA, thus
 CC proving that the recombinant human DNA polymerase alpha is useful as a
 CC reagent for screening analogues. See also AAQ40921-49. (Updated on 25-MAR
 CC -2003 to correct PN field.)

XX Sequence 16 BP; 3 A; 6 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CTCTGCCCGCTGG 24
 DB 16 CTCTGCCCGCTGG 4

RESULT 242

AAQ4099
 ID AAX04099 standard; DNA; 16 BP.

XX AC AAX04099;

XX 12-APR-1999 (first entry)

XX PUR element conservation oligonucleotide #7.

XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
 KW monoclonal antibody; identification; characterisation; ss.

XX Synthetic.

XX US5869622-A.

XX 09-FEB-1999.

XX 07-JUN-1995; 95US-00486809.

XX 28-AUG-1992; 92US-00938189.

XX 02-FEB-1993; 93US-00014943.

XX 06-JUN-1995; 95US-00470911.

XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX Bergemann AD, Johnson EM;

XX WPI; 1999-152881/13.

XX Monoclonal antibody specific for PUR protein - useful for treating
 PT cancer.

XX Disclosure; Col 13; 64pp; English.

XX The present invention describes a monoclonal antibody that specifically
 CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR
 CC protein and neutralise PUR activity may be used to treat
 CC hyperproliferative diseases such as cancer. PUR antibodies may be used
 CC diagnostically to detect aberrant expression of the PUR protein and/or
 CC mutations in the PUR gene. The present sequence represents an
 CC oligonucleotide from the present invention

XX Sequence 16 BP; 6 A; 0 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1383 GAGGAGGAGGAGG 1395

DB 2 GAGGAGGAGGAGG 14

RESULT 243

ABZ72358/C

ID ABZ72358 standard; DNA; 16 BP.

XX AC ABZ72358;

XX 03-APR-2003 (first entry)

XX Gene 216 polymorphism genotyping ASO primer SEQ ID NO 330.

XX Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
 KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
 KW obesity; inflammatory bowel disease; primer; ss.

XX Synthetic.

XX WO200178894-A2.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2004, 09:51:10 ; Search time 7 Seconds
(without alignments)

1.692 Million cell updates/sec

Title: US-09-817-538-2

Perfect score: 1611

Sequence: 1 atgtcggggtctctgcgcg.....tcctcaogttttttccccc 1611

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 194 seqs, 3677 residues

Total number of hits satisfying chosen parameters: 388

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 194 summaries

Database : rge2.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	26	1.6	26	1	BD244917
C 2	26	1.6	26	1	AX053080
C 3	26	1.6	26	1	AX053089
C 4	26	1.6	26	1	AX053098
C 5	26	1.6	26	1	AX053088
C 6	25	1.6	26	1	AX053078
C 7	25	1.6	26	1	AX053079
C 8	24.4	1.5	26	1	AX053087
C 9	24.4	1.5	26	1	AX053088
C 10	24.4	1.5	26	1	AX053088
C 11	23.4	1.5	26	1	AX053088
C 12	23.4	1.5	26	1	AX053088
C 13	23.4	1.5	26	1	AX053088
C 14	23.4	1.5	26	1	AX053088
C 15	23.4	1.5	26	1	AX053088
C 16	23.4	1.5	26	1	AX053088
C 17	23.4	1.5	26	1	AX053088
C 18	23.4	1.5	26	1	AX053088
C 19	22.8	1.4	26	1	AX053088
C 20	22.8	1.4	26	1	AX053088
C 21	22.8	1.4	26	1	AX053088
C 22	22.8	1.4	26	1	AX053088
C 23	22.8	1.4	26	1	AX053088
C 24	22.8	1.4	26	1	AX053088
C 25	22.8	1.4	26	1	AX053088
C 26	22.8	1.4	26	1	AX053088
C 27	21.8	1.4	26	1	AX053088
C 28	21.8	1.4	26	1	AX053088
C 29	21.4	1.3	23	1	BD244920
C 30	21.4	1.3	23	1	BD244921
C 31	21.4	1.3	23	1	AX053088
C 32	21.4	1.3	23	1	AX053088
C 33	20.4	1.3	22	1	BD244922

C 34	20.4	1.3	22	1	AX546305
C 35	20.4	1.3	22	1	AX546395
C 36	20	1.2	20	1	BD244905
C 37	20	1.2	20	1	BD244906
C 38	20	1.2	20	1	BD244907
C 39	20	1.2	20	1	BD244908
C 40	20	1.2	20	1	BD244909
C 41	20	1.2	20	1	BD244910
C 42	20	1.2	20	1	BD244911
C 43	20	1.2	20	1	BD244912
C 44	20	1.2	20	1	BD244913
C 45	20	1.2	20	1	BD244914
C 46	20	1.2	20	1	BD244915
C 47	20	1.2	20	1	BD244916
C 48	20	1.2	20	1	BD244917
C 49	20	1.2	20	1	BD244918
C 50	20	1.2	20	1	BD244919
C 51	20	1.2	20	1	BD244920
C 52	20	1.2	20	1	BD244921
C 53	20	1.2	20	1	BD244922
C 54	20	1.2	20	1	BD244923
C 55	20	1.2	20	1	BD244924
C 56	20	1.2	20	1	BD244925
C 57	20	1.2	20	1	BD244926
C 58	20	1.2	20	1	BD244927
C 59	20	1.2	20	1	BD244928
C 60	20	1.2	20	1	BD244929
C 61	20	1.2	20	1	BD244930
C 62	20	1.2	20	1	BD244931
C 63	20	1.2	20	1	BD244932
C 64	20	1.2	20	1	BD244933
C 65	20	1.2	20	1	BD244934
C 66	19.2	1.1	24	1	AX173370
C 67	18.4	1.1	20	1	AX546376
C 68	18.4	1.1	20	1	AX546377
C 69	18.4	1.1	20	1	AX546378
C 70	18.4	1.1	20	1	AX546379
C 71	18.4	1.1	20	1	AX546380
C 72	17	1.1	17	1	AX703613
C 73	17	1.1	17	1	AX703614
C 74	16.8	1.0	20	1	BD244910
C 75	16.8	1.0	20	1	AX546265
C 76	16.4	1.0	20	1	AX029137
C 77	16.4	1.0	20	1	AX036521
C 78	16.4	1.0	20	1	AX073958
C 79	16.4	1.0	20	1	AX096054
C 80	16.4	1.0	20	1	AX105513
C 81	16.4	1.0	20	1	AX105513
C 82	16.4	1.0	20	1	AX105513
C 83	16.4	1.0	20	1	AX105513
C 84	16.4	1.0	20	1	AX105513
C 85	16.4	1.0	20	1	AX105513
C 86	16.4	1.0	20	1	AX105513
C 87	16.4	1.0	20	1	AX105513
C 88	16.4	1.0	20	1	AX105513
C 89	16.4	1.0	20	1	AX105513
C 90	16.4	1.0	20	1	AX105513
C 91	16.4	1.0	20	1	AX105513
C 92	16.4	1.0	20	1	AX105513
C 93	16.4	1.0	20	1	AX105513
C 94	16.4	1.0	20	1	AX105513
C 95	16.4	1.0	20	1	AX105513
C 96	16.4	1.0	20	1	AX105513
C 97	16.4	1.0	20	1	AX105513
C 98	16.4	1.0	20	1	AX105513
C 99	16.4	1.0	20	1	AX105513
C 100	16.4	1.0	20	1	AX105513
C 101	16.4	1.0	20	1	AX105513
C 102	16.4	1.0	20	1	AX105513
C 103	16.4	1.0	20	1	AX105513
C 104	16.4	1.0	20	1	AX105513
C 105	16.4	1.0	20	1	AX105513
C 106	16.4	1.0	20	1	AX105513

C 107	14.4	0.9	0.9	17	1	AX217646	ACCESSION:AX217646
C 108	14.4	0.9	0.9	17	1	AX218225	ACCESSION:AX218225
C 109	14.4	0.9	0.9	17	1	AX475558	ACCESSION:AX475558
C 110	14.4	0.9	0.9	17	1	AX475559	ACCESSION:AX475559
C 111	14.4	0.9	0.9	17	1	AX784017	ACCESSION:AX784017
C 112	14.4	0.9	0.9	17	1	AX784018	ACCESSION:AX784018
C 113	14.4	0.9	0.9	17	1	AX784019	ACCESSION:AX784019
C 114	14.4	0.9	0.9	17	1	AX784020	ACCESSION:AX784020
C 115	14.4	0.9	0.9	17	1	AX784021	ACCESSION:AX784021
C 116	14.4	0.9	0.9	17	1	AX784022	ACCESSION:AX784022
C 117	14.4	0.9	0.9	17	1	AX784023	ACCESSION:AX784023
C 118	14.4	0.9	0.9	17	1	AX784024	ACCESSION:AX784024
C 119	14.4	0.9	0.9	17	1	AX784025	ACCESSION:AX784025
C 120	13.8	0.9	0.9	17	1	AX784026	ACCESSION:AX784026
C 121	13.8	0.9	0.9	17	1	AX784027	ACCESSION:AX784027
C 122	13.8	0.9	0.9	17	1	AX784028	ACCESSION:AX784028
C 123	13.8	0.9	0.9	17	1	AX784029	ACCESSION:AX784029
C 124	13.8	0.9	0.9	17	1	AX784030	ACCESSION:AX784030
C 125	13.8	0.9	0.9	17	1	AX784031	ACCESSION:AX784031
C 126	13.8	0.9	0.9	17	1	AX784032	ACCESSION:AX784032
C 127	13.8	0.9	0.9	17	1	AX784033	ACCESSION:AX784033
C 128	13.8	0.9	0.9	17	1	AX784034	ACCESSION:AX784034
C 129	13.8	0.9	0.9	17	1	AX784035	ACCESSION:AX784035
C 130	13.8	0.9	0.9	17	1	AX784036	ACCESSION:AX784036
C 131	13.8	0.9	0.9	17	1	AX784037	ACCESSION:AX784037
C 132	13.8	0.9	0.9	17	1	AX784038	ACCESSION:AX784038
C 133	13.8	0.9	0.9	17	1	AX784039	ACCESSION:AX784039
C 134	13.8	0.9	0.9	17	1	AX784040	ACCESSION:AX784040
C 135	13.8	0.9	0.9	17	1	AX784041	ACCESSION:AX784041
C 136	13.8	0.9	0.9	17	1	AX784042	ACCESSION:AX784042
C 137	13.8	0.9	0.9	17	1	AX784043	ACCESSION:AX784043
C 138	13.8	0.9	0.9	17	1	AX784044	ACCESSION:AX784044
C 139	13.8	0.9	0.9	17	1	AX784045	ACCESSION:AX784045
C 140	13.8	0.9	0.9	17	1	AX784046	ACCESSION:AX784046
C 141	13.8	0.9	0.9	17	1	AX784047	ACCESSION:AX784047
C 142	13.8	0.9	0.9	17	1	AX784048	ACCESSION:AX784048
C 143	13.8	0.9	0.9	17	1	AX784049	ACCESSION:AX784049
C 144	13.8	0.9	0.9	17	1	AX784050	ACCESSION:AX784050
C 145	13.8	0.9	0.9	17	1	AX784051	ACCESSION:AX784051
C 146	13.8	0.9	0.9	17	1	AX784052	ACCESSION:AX784052
C 147	13.8	0.9	0.9	17	1	AX784053	ACCESSION:AX784053
C 148	13.8	0.9	0.9	17	1	AX784054	ACCESSION:AX784054
C 149	13.8	0.9	0.9	17	1	AX784055	ACCESSION:AX784055
C 150	13.8	0.9	0.9	17	1	AX784056	ACCESSION:AX784056
C 151	13.8	0.9	0.9	17	1	AX784057	ACCESSION:AX784057
C 152	13.8	0.9	0.9	17	1	AX784058	ACCESSION:AX784058
C 153	13.8	0.9	0.9	17	1	AX784059	ACCESSION:AX784059
C 154	13.8	0.9	0.9	17	1	AX784060	ACCESSION:AX784060
C 155	13.8	0.9	0.9	17	1	AX784061	ACCESSION:AX784061
C 156	13.8	0.9	0.9	17	1	AX784062	ACCESSION:AX784062
C 157	13.8	0.9	0.9	17	1	AX784063	ACCESSION:AX784063
C 158	13.8	0.9	0.9	17	1	AX784064	ACCESSION:AX784064
C 159	13.8	0.9	0.9	17	1	AX784065	ACCESSION:AX784065
C 160	13.8	0.9	0.9	17	1	AX784066	ACCESSION:AX784066
C 161	13.4	0.8	0.8	16	1	AX784067	ACCESSION:AX784067
C 162	13.4	0.8	0.8	16	1	AX784068	ACCESSION:AX784068
C 163	13.4	0.8	0.8	16	1	AX784069	ACCESSION:AX784069
C 164	13.4	0.8	0.8	16	1	AX784070	ACCESSION:AX784070
C 165	13.4	0.8	0.8	16	1	AX784071	ACCESSION:AX784071
C 166	13.4	0.8	0.8	16	1	AX784072	ACCESSION:AX784072
C 167	13.4	0.8	0.8	16	1	AX784073	ACCESSION:AX784073
C 168	13.4	0.8	0.8	16	1	AX784074	ACCESSION:AX784074
C 169	13.4	0.8	0.8	16	1	AX784075	ACCESSION:AX784075
C 170	13.4	0.8	0.8	16	1	AX784076	ACCESSION:AX784076
C 171	13.4	0.8	0.8	16	1	AX784077	ACCESSION:AX784077
C 172	13.4	0.8	0.8	16	1	AX784078	ACCESSION:AX784078
C 173	13.4	0.8	0.8	16	1	AX784079	ACCESSION:AX784079
C 174	13.4	0.8	0.8	16	1	AX784080	ACCESSION:AX784080
C 175	13.4	0.8	0.8	16	1	AX784081	ACCESSION:AX784081
C 176	13.4	0.8	0.8	16	1	AX784082	ACCESSION:AX784082
C 177	13.4	0.8	0.8	16	1	AX784083	ACCESSION:AX784083
C 178	13.4	0.8	0.8	16	1	AX784084	ACCESSION:AX784084
C 179	13.4	0.8	0.8	16	1	AX784085	ACCESSION:AX784085

ALIGNMENTS

RESULT 1	BD244917/c	26 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD244917	Modulation of gene expression by combination therapy.			
DEFINITION	BD244917	Modulation of gene expression by combination therapy.			
ACCESSION	BD244917	GI:33054687			
VERSION	BD244917.1	JP 2002528391-A/45.			
KEYWORDS	JP 2002528391-A/45.	synthetic construct			
SOURCE	JP 2002528391-A/45.	artificial constructs.			
ORGANISM	JP 2002528391-A/45.	artificial sequences.			
REFERENCE	JP 2002528391-A/45.	1 (bases 1 to 26)			
AUTHORS	Besterman,J.M., Macleod,A.R. and Siders,W.M.				
TITLE	Modulation of gene expression by combination therapy.				
JOURNAL	Patent: JP 2002528391-A 45 03-SEP-2002;				
COMMENT	METHYLENE INC				
OS	Artificial Sequence				
PN	JP 2002528391-A/45				
PD	03-SEP-2002				
PF	19-OCT-1999 JP 2000576885				
PI	19-OCT-1998 US 60/104804				
PT	JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC				
PC	A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/706,				
PC	A61K31/7068,A61K31/7089,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC				
PC	09//				
CC	C12N5/10,C12N15/00,C12N5/00				
CC	antisense				
FT	Key	Location/Qualifiers			
FT	source	1..26			
FT	source	/organism='Artificial Sequence'.			
FEATURES	source				
Query Match	1.6%; Score 26; DB 1; Length 26;				
Best Local Similarity	100.0%; Pred. No. 8.9;				
Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	211 GAATCCGATGACTCAATTAATTTGCTG 236				
DB	26 GAATCCGATGACTCAATTAATTTGCTG 1				
RESULT 2	AX053080/c	26 bp	DNA	linear	PAT 12-JAN-2001
LOCUS	AX053080	Sequence 4 from Patent WO0071703.			
DEFINITION	AX053080	Sequence 4 from Patent WO0071703.			
ACCESSION	AX053080	GI:12227137			
VERSION	AX053080.1				
KEYWORDS	AX053080.1				

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1
Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 4 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers

source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 3
AX053089/c
LOCUS AX053089 26 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 13 from Patent WO0071703.
ACCESSION AX053089
VERSION AX053089.1 GI:12227146
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1
Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 13 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers

source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions 1-4 and 23-26 are 2'-methoxyribose substituted nucleotides; positions 5-22 are deoxyribonucleotides"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 4
AX546298/c
LOCUS AX546298 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 47 from Patent EP1243290.
ACCESSION AX546298
VERSION AX546298.1 GI:25811489
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1
Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 47 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers

source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 5
AX546388/c
LOCUS AX546388 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 47 from Patent EP1243289.
ACCESSION AX546388
VERSION AX546388.1 GI:25811579
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1
Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 47 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers

source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.6%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAATTGCTG 236
Db 26 GAATCCGCATGACTCATAATTGCTG 1

RESULT 6
AX546341/c
LOCUS AX546341 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 90 from Patent EP1243290.
ACCESSION AX546341
VERSION AX546341.1 GI:25811532
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1
Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 90 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES Location/Qualifiers

source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAATTGCTG 236

Db 25 AATCCGCATGACTCATATTGCTG 1
|||||
AX546431/c 26 bp DNA linear PAT 26-NOV-2002
LOCUS Sequence 90 from Patent EP1243289.
DEFINITION
ACCESSION AX546431
VERSION AX546431.1 GI:25811622
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 90 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.6%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 212 AATCCGCATGACTCATATTGCTG 236
|||||
Db 25 AATCCGCATGACTCATATTGCTG 1
|||||
RESULT 8
AX053078/c 26 bp DNA linear PAT 12-JAN-2001
LOCUS Sequence 2 from Patent WO0071703.
DEFINITION
ACCESSION AX053078
VERSION AX053078.1 GI:12227135
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 2 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 211 GAATCCGCATGACTCATATTGCTG 236
|||||
Db 26 GAATCCGCATGACCCCATATTGCTG 1
|||||
RESULT 11
AX053088/c 26 bp DNA linear PAT 12-JAN-2001
LOCUS Sequence 12 from Patent WO0071703.
DEFINITION
ACCESSION AX053088
VERSION AX053088.1 GI:12227145
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 12 30-NOV-2000;
Methylgene, Inc. (CA)
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 3 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 211 GAATCCGCATGACTCATATTGCTG 236
|||||
Db 26 GAATCCGCATGACCCCATATTGCTG 1
|||||
RESULT 10
AX053087/c 26 bp DNA linear PAT 12-JAN-2001
LOCUS Sequence 11 from Patent WO0071703.
DEFINITION
ACCESSION AX053087
VERSION AX053087.1 GI:12227144
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 11 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions 1-4 and 23-26 are 2'-methoxyribose substituted nucleotides; positions 5-22 are deoxyribonucleotides"

FEATURES
source
Location/Qualifiers
1..26
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Description of Combined DNA/RNA Molecule: Positions 1-4 and 23-26 are 2'-methoxyribose substituted nucleotides; positions 5-22 are deoxyribonucleotides"

Query Match 1.5%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 211 GAATCCGCATGACTCATAAATTGCTG 236
Db 26 GAATCCGCATGACTCATAAATTGCTG 1

RESULT 12
AX546333/c
LOCUS AX546333 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 82 from Patent EP1243290.
ACCESSION AX546333
VERSION AX546333.1 GI:25811524
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 82 25-SEP-2002;
Methylgene, Inc. (CA)

FEATURES
source
Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 19;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAAATTGCTG 236
Db 25 AATCCGCATGACCCATAAATTGCTG 1

RESULT 13
AX546334/c
LOCUS AX546334 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 83 from Patent EP1243290.
ACCESSION AX546334
VERSION AX546334.1 GI:25811525
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 83 25-SEP-2002;
Methylgene, Inc. (CA)

FEATURES
source
Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAAATTGCTG 236
Db 25 AATCCGCATGACCCATAAATTGCTG 1

RESULT 14
AX546423/c
LOCUS AX546423 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 82 from Patent EP1243289.
ACCESSION AX546423
VERSION AX546423.1 GI:25811614
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 82 25-SEP-2002;
Methylgene, Inc. (CA)

FEATURES
source
Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 19;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAAATTGCTG 236
Db 25 AATCCGCATGACCCATAAATTGCTG 1

RESULT 15
AX546424/c
LOCUS AX546424 26 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 83 from Patent EP1243289.
ACCESSION AX546424
VERSION AX546424.1 GI:25811615
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 83 25-SEP-2002;
Methylgene, Inc. (CA)

FEATURES
source
Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.5%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 19;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 212 AATCCGCATGACTCATAAATTGCTG 236
Db 25 AATCCGCATGACCCATAAATTGCTG 1

RESULT 16
BD244915/c
LOCUS BD244915 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy

```

ACCESSION BD244915
VERSION BD244915.1 GI:33054685
KEYWORDS JP 2002528391-A/43.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 43 03-SEP-2002;
METHYLENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/43
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1..23
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="oligonucleotide"
FEATURES
source
Query Match 1..4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 AAAGTCTGTTACTACTACGACGG 160
DB 23 AAAGTCTGTTACTACTACGACGG 1
RESULT 17
AX546296/c
LOCUS 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Modulation of gene expression by combination therapy
ACCESSION AX546296
VERSION AX546296.1 GI:25811487
KEYWORDS synthetic construct
SOURCE synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 45 25-SEP-2002;
Methyigene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"
Query Match 1..4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 AAAGTCTGTTACTACTACGACGG 160
DB 23 AAAGTCTGTTACTACTACGACGG 1
RESULT 18
AX546386/c
LOCUS 23 bp DNA linear PAT 26-NOV-2002
DEFINITION Modulation of gene expression by combination therapy
ACCESSION AX546386
VERSION AX546386.1 GI:25811577
KEYWORDS synthetic construct
SOURCE synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 45 25-SEP-2002;
Methyigene, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"
Query Match 1..4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 AAAGTCTGTTACTACTACGACGG 160
DB 23 AAAGTCTGTTACTACTACGACGG 1
RESULT 19
BD244923/c
LOCUS 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy
ACCESSION BD244923
VERSION BD244923.1 GI:33054693
KEYWORDS JP 2002528391-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 51 03-SEP-2002;
METHYLENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/51
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1..26
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"
FEATURES
source
Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1..4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 211 GAATCGCATGACTCATTAATTGCTG 236

```

```

Db      26 GAATCCGCATGACCCATACTTGCTG 1
|||||
RESULT 20
AX053081/c
LOCUS      AX053081          26 bp      DNA      linear      PAT 12-JAN-2001
DEFINITION Sequence 5 from Patent WO0071703.
ACCESSION  AX053081
VERSION     AX053081.1  GI:12227138
KEYWORDS
SOURCE      synthetic construct
            artificial sequences.
REFERENCE
AUTHORS     Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE       Inhibition of histone deacetylase
JOURNAL     Patent: WO 0071703-A 5 30-NOV-2000;
            Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match      1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      211 GAATCCGCATGACTCATATTTGCTG 236
|||||
Db      26 GAATCCGCATGACCCATACTTGCTG 1
|||||

RESULT 21
AX053090/c
LOCUS      AX053090          26 bp      DNA      linear      PAT 12-JAN-2001
DEFINITION Sequence 14 from Patent WO0071703.
ACCESSION  AX053090
VERSION     AX053090.1  GI:12227147
KEYWORDS
SOURCE      synthetic construct
            artificial sequences.
REFERENCE
AUTHORS     Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE       Inhibition of histone deacetylase
JOURNAL     Patent: WO 0071703-A 14 30-NOV-2000;
            Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions
1-4 and 23-26 are 2'-methoxyribose substituted
nucleotides; positions 5-22 are deoxyribonucleotides"

Query Match      1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      211 GAATCCGCATGACTCATATTTGCTG 236
|||||
Db      26 GAATCCGCATGACCCATACTTGCTG 1
|||||

RESULT 22
AX546306/c
LOCUS      AX546306          26 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 55 from Patent EP1243289.
ACCESSION  AX546306
VERSION     AX546306.1  GI:25811587
KEYWORDS
SOURCE      synthetic construct
            artificial sequences.
REFERENCE
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243289-A 55 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match      1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      211 GAATCCGCATGACTCATATTTGCTG 236
|||||
Db      26 GAATCCGCATGACCCATACTTGCTG 1
|||||

RESULT 23
AX546396/c
LOCUS      AX546396          26 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 55 from Patent EP1243289.
ACCESSION  AX546396
VERSION     AX546396.1  GI:25811587
KEYWORDS
SOURCE      synthetic construct
            artificial sequences.
REFERENCE
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243289-A 55 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match      1.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      211 GAATCCGCATGACTCATATTTGCTG 236
|||||
Db      26 GAATCCGCATGACCCATACTTGCTG 1
|||||

RESULT 24
BD244916/c
LOCUS      BD244916          22 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION  BD244916
VERSION     BD244916.1  GI:33054686
KEYWORDS   JP 2002528391-A/44.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: JP 2002528391-A 44 03-SEP-2002;
            METHYLGENE INC
COMMENT     OS Artificial Sequence

```


Best Local Similarity 92.0%; Pred. No. 29;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 212 AATCCGATGACTCATATTTGCTG 236
|||||
Db 25 AATCCGATGACCATTAATTGCTG 1
|||||

RESULT 29
BD244920/c
LOCUS BD244920.1 GI:33054690
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION JP 2002528391-A/48
VERSION JP 2002528391-A/48
KEYWORDS synthetic construct
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 23)
REFERENCE 1 (bases 1 to 23)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 48 03-SEP-2002;
METHYLGENE INC

COMMENT
OS Artificial Sequence
PN JP 2002528391-A/48
PD 03-SEP-2002
PR 19-OCT-1999 JP 2000576885
PI 19-OCT-1998 US 60/104804
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..23
FT source /organism='Artificial Sequence'
FT Location/Qualifiers
1..23
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAGTCTGTACTACTACGACGG 160
|||||
Db 23 AAGTCTGTACTACTACGACGG 1
|||||

RESULT 31
AX546304/c
LOCUS AX546304.1 GI:25811495
DEFINITION Sequence 53 from Patent EP1243290.
ACCESSION AX546304
VERSION AX546304.1 GI:25811495
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 53 25-SEP-2002;
Methylgene, Inc. (CA)

FEATURES
source
1..23
/organism='synthetic construct'
/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='oligonucleotide'

Query Match 1.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAGTCTGTACTACTACGACGG 160
|||||
Db 23 AAGTCTGTACTACTACGACGG 1
|||||

RESULT 32
AX546394/c
LOCUS AX546394.1 GI:25811585
DEFINITION Sequence 53 from Patent EP1243289.
ACCESSION AX546394
VERSION AX546394.1 GI:25811585
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 53 25-SEP-2002;
Methylgene, Inc. (CA)

```

FEATURES             Location/Qualifiers
     source
     1..23
     /organism="synthetic construct"
     /mol_type="unassigned DNA"
     /db_xref="taxon:32630"
     /note="oligonucleotide"

Query Match
Best Local Similarity 1.3%; Score 21.4; DB 1; Length 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAGTCTGTTACTACTACGACGG 160
Db 23 AAGTCTGTTACTACTACGACGG 1

RESULT 33
BD244922/c
LOCUS BD244922 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244922
VERSION BD244922.1 GI:33054692
KEYWORDS JP 2002528391-A/50.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 22)
Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: JP 2002528391-A 50 03-SEP-2002;
JOURNAL METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/50
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
CC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key 1..22
FT source Location/Qualifiers
FT Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES             Location/Qualifiers
     source
     1..22
     /organism="synthetic construct"
     /mol_type="synthetic construct"
     /db_xref="taxon:32630"
     /note="oligonucleotide"

Query Match
Best Local Similarity 1.3%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGGACA 187
Db 22 TTGGAATTTACTATTATGGACA 1

RESULT 34
AX546305/c
LOCUS BD244905 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244905
VERSION BD244905.1 GI:33054675
KEYWORDS JP 2002528391-A/33.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 20)
Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: JP 2002528391-A 33 03-SEP-2002;
JOURNAL METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/33
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
CC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key 1..22
FT source Location/Qualifiers
FT Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES             Location/Qualifiers
     source
     1..22
     /organism="synthetic construct"
     /mol_type="synthetic construct"
     /db_xref="taxon:32630"
     /note="oligonucleotide"

Query Match
Best Local Similarity 1.3%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGGACA 187
Db 22 TTGGAATTTACTATTATGGACA 1

RESULT 35
AX546395/c
LOCUS AX546395 22 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 54 from Patent EP1243289.
ACCESSION AX546395
VERSION AX546395.1 GI:25811586
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1
Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: EP 1243289-A 54 25-SEP-2002;
JOURNAL METHYLGENE, INC. (CA)
COMMENT OS Artificial Sequence
PN EP 1243289-A/54
PD 25-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
CC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key 1..22
FT source Location/Qualifiers
FT Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES             Location/Qualifiers
     source
     1..22
     /organism="synthetic construct"
     /mol_type="synthetic construct"
     /db_xref="taxon:32630"
     /note="oligonucleotide"

Query Match
Best Local Similarity 1.3%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGGACA 187
Db 22 TTGGAATTTACTATTATGGACA 1

RESULT 36
BD244905/c
LOCUS BD244905 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244905
VERSION BD244905.1 GI:33054675
KEYWORDS JP 2002528391-A/33.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 20)
Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: JP 2002528391-A 33 03-SEP-2002;
JOURNAL METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/33
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
CC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key 1..22
FT source Location/Qualifiers
FT Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES             Location/Qualifiers
     source
     1..22
     /organism="synthetic construct"
     /mol_type="synthetic construct"
     /db_xref="taxon:32630"
     /note="oligonucleotide"

Query Match
Best Local Similarity 1.3%; Score 21.4; DB 1; Length 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 138 AAGTCTGTTACTACTACGACGG 160
Db 23 AAGTCTGTTACTACTACGACGG 1

RESULT 33
BD244922/c
LOCUS BD244922 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244922
VERSION BD244922.1 GI:33054692
KEYWORDS JP 2002528391-A/50.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 22)
Besterman,J.M., Macleod,A.R. and Siders,W.M.
AUTHORS Modulation of gene expression by combination therapy
TITLE Patent: JP 2002528391-A 50 03-SEP-2002;
JOURNAL METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/50
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
CC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key 1..22
FT source Location/Qualifiers
FT Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES             Location/Qualifiers
     source
     1..22
     /organism="synthetic construct"
     /mol_type="synthetic construct"
     /db_xref="taxon:32630"
     /note="oligonucleotide"

Query Match
Best Local Similarity 1.3%; Score 20.4; DB 1; Length 22;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 166 TTGGAATTTACTATTATGGACA 187
Db 22 TTGGAATTTACTATTATGGACA 1

RESULT 34
AX546305/c
LOCUS BD244905 22 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 54 from Patent EP1243290.
ACCESSION AX546305
VERSION AX546305.1 GI:25811496
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1

```

706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/00, C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 CCCGCTGGTGTCTGCTCTC 36
Db 20 CCCGCTGGTGTCTGCTCTC 1
RESULT 37
BD244906/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244906
VERSION BD244906.1 GI:33054676
KEYWORDS JP 2002528391-A/34
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 34 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/34
PD 03-SEP-2002
PF 19-OCT-1998 US 60/104804
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 GCTGCTCCCACTCGGTCTAT 48
Db 20 GCTGCTCCCACTCGGTCTAT 1
RESULT 38
BD244907/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244907
VERSION BD244907.1 GI:33054677
KEYWORDS JP 2002528391-A/35
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 35 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/35
PD 03-SEP-2002
PF 19-OCT-1998 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 31 TGTCTCCCACTCGGTCTATCC 50
Db 20 TGTCTCCCACTCGGTCTATCC 1
RESULT 39
BD244908/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244908
VERSION BD244908.1 GI:33054678
KEYWORDS JP 2002528391-A/36
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 36 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/36
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 29 GCTGCTCCCACTCGGTCTAT 48
Db 20 GCTGCTCCCACTCGGTCTAT 1
RESULT 38
BD244907/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244907
VERSION BD244907.1 GI:33054677
KEYWORDS JP 2002528391-A/35
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 35 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/35
PD 03-SEP-2002
PF 19-OCT-1998 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244907
VERSION BD244907.1 GI:33054677
KEYWORDS JP 2002528391-A/35
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 35 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/35
PD 03-SEP-2002
PF 19-OCT-1998 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 31 TGTCTCCCACTCGGTCTATCC 50
Db 20 TGTCTCCCACTCGGTCTATCC 1
RESULT 39
BD244908/c
LOCUS
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244908
VERSION BD244908.1 GI:33054678
KEYWORDS JP 2002528391-A/36
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 36 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/36
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC
A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense Location/Qualifiers
FH Key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'


```
FT          /organism='Artificial Sequence'.
FEATURES
  source    Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCCTG 52
    |||||
Db 20 TCTCCCACTCGGTCATCCTG 1

RESULT 40
BD244909/c
LOCUS      20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION  BD244909
VERSION     BD244909.1 GI:33054679
KEYWORDS   JP 2002528391-A/37.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL    METHYLGENE INC
COMMENT    OS Artificial Sequence
            PN JP 2002528391-A/37
            PD 03-SEP-2002
            PF 19-OCT-1999 JP 2000576885
            PR 19-OCT-1998 US 60/104804
            PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
            A61K48/00,A61K31/165,A61K31/513,A61K31/517,A61K31/ PC
            706,
            PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
            09//
            C12N5/10,C12N15/00,C12N5/00
            CC antisense Location/Qualifiers
            FH Key 1..20
            FT source /organism='Artificial Sequence'.
FEATURES
  source    Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1504 CCAAGGAGGAGAGCCAGAA 1523
    |||||
Db 20 CCAAGGAGGAGAGCCAGAA 1

RESULT 42
BD244913/c
LOCUS      20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION  BD244913
VERSION     BD244913.1 GI:33054683
KEYWORDS   JP 2002528391-A/41.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL    METHYLGENE INC
COMMENT    OS Artificial Sequence
            PN JP 2002528391-A/41
            PD 03-SEP-2002
            PF 19-OCT-1999 JP 2000576885
            PR 19-OCT-1998 US 60/104804
            PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
            A61K48/00,A61K31/165,A61K31/513,A61K31/517,A61K31/ PC
            706,
            PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
            09//
            C12N5/10,C12N15/00,C12N5/00
            CC antisense Location/Qualifiers
            FH Key 1..20
            FT source /organism='Artificial Sequence'.
FEATURES
  source    Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTCATCCTCGAGAACACA 60
    |||||
Db 20 TCGGTCATCCTCGAGAACACA 1

RESULT 41
BD244911/c
LOCUS      20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION  BD244911
VERSION     BD244911.1 GI:33054681
KEYWORDS   JP 2002528391-A/39.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
```

```

Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGTTTC 1584
    |||||
Db 20 CCTCTCCAGCTCTGGTTTC 1

RESULT 43
BD244914/c 20 bp DNA linear PAT 17-JUL-2003
LOCUS Modulation of gene expression by combination therapy.
DEFINITION
ACCESSION BD244914
VERSION BD244914.1 GI:33054684
KEYWORDS JP 2002528391-A/42;
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 42 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/42
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PI 19-OCT-1998 US 60/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A1K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1..20
FT /organism="Artificial Sequence".
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
    |||||
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 44
AX053077/c 20 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0071703.
ACCESSION AX053077
VERSION AX053077.1 GI:12227134
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 1 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"

```

```

/db_xref="taxon:32630"
/note="synthetic oligonucleotide"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
    |||||
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 45
AX053086/c 20 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 10 from Patent WO0071703.
ACCESSION AX053086
VERSION AX053086.1 GI:12227143
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE Inhibition of histone deacetylase
JOURNAL Patent: WO 0071703-A 10 30-NOV-2000;
Methylgene, Inc. (CA)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule: Positions
1-4 and 17-20 are 2'-methoxyribose substituted
nucleotides; positions 5-16 are deoxyribonucleotides"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
    |||||
Db 20 TGCTGAGTCCCTCAGTTTC 1

RESULT 46
AX456071/c 20 bp DNA linear PAT 06-JUL-2002
LOCUS
DEFINITION Sequence 1 from Patent WO0170675.
ACCESSION AX456071
VERSION AX456071.1 GI:21715026
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1
AUTHORS Delorme,D., Woo,S.H. and Vaisburg,A.
TITLE Inhibitors of histone deacetylase
JOURNAL Patent: WO 0170675-A 1 27-SEP-2001;
Methylgene, Inc. (CA)
FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1585 TGCTGAGTCCCTCAGTTTC 1604
    |||||

```

```
Db      20  TGCTGAGTCCTCAGCTTTC 1

RESULT 47
AX546072/c
LOCUS      AX546072      20 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 2 from Patent WO0170675.
ACCESSION  AX546072
VERSION     AX546072.1  GI:21715027
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Delorme,D., Woo,S.H. and Vaisburg,A.
TITLE       Inhibitors of histone deacetylase
JOURNAL     Patent: WO 0170675-A 2 27-SEP-2001;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1565  CCTCTCCAGCTCGGCTTC 1584
            |||||
Db      20  CCTCTCCAGCTCGGCTTC 1

RESULT 48
AX546286/c
LOCUS      AX546286      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 35 from Patent EP1243290.
ACCESSION  AX546286
VERSION     AX546286.1  GI:25811477
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Besterman,J.M., Macleod,A.R. and Siders,W.M.
REFERENCE   1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 35 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17  CCGCTGGTGTCTGTCTC 36
            |||||
Db      20  CCGCTGGTGTCTGTCTC 1

RESULT 49
AX546287/c
LOCUS      AX546287      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 36 from Patent EP1243290.
ACCESSION  AX546287
VERSION     AX546287.1  GI:25811478
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 36 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"

ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 36 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      31  TGTCTCCACTCGGTCTATCC 50
            |||||
Db      20  TGTCTCCACTCGGTCTATCC 1

RESULT 51
AX546289/c
LOCUS      AX546289      20 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 38 from Patent EP1243290.
ACCESSION  AX546289
VERSION     AX546289.1  GI:25811480
KEYWORDS    synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Besterman,J.M., Macleod,A.R. and Siders,W.M.
REFERENCE   1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 38 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"

ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 38 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"

ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE       Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 38 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
            source
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /note="oligonucleotide"

Query Match      1.2%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      31  TGTCTCCACTCGGTCTATCC 50
            |||||
Db      20  TGTCTCCACTCGGTCTATCC 1
```

[illegible]

<hr/>					
/db_xref="taxon:32630" /note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 33 TCTCCACTCGGTCACTG 52					
DB 20 TCTCCACTCGGTCACTG 1					
RESULT 52					
AX546290/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 41 TCGTCATCTCGAGAACACA 60					
DB 20 TCGTCATCTCGAGAACACA 1					
RESULT 53					
AX546292/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1585 TGCTGAGTCCCTCAGTTTC 1604					
DB 20 TGCTGAGTCCCTCAGTTTC 1					
RESULT 54					
AX546294/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1585 TGCTGAGTCCCTCAGTTTC 1604					
DB 20 TGCTGAGTCCCTCAGTTTC 1					
RESULT 55					
AX546295/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1585 TGCTGAGTCCCTCAGTTTC 1604					
DB 20 TGCTGAGTCCCTCAGTTTC 1					
RESULT 56					
AX546376/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1504 CCAAGGAGGAGGCCAGAA 1523					
DB 20 CCAAGGAGGAGGCCAGAA 1					
RESULT 57					
AX546377/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1504 CCAAGGAGGAGGCCAGAA 1523					
DB 20 CCAAGGAGGAGGCCAGAA 1					
RESULT 58					
AX546378/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1504 CCAAGGAGGAGGCCAGAA 1523					
DB 20 CCAAGGAGGAGGCCAGAA 1					
RESULT 59					
AX546379/c					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1. .20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity 1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1504 CCAAGGAGGAGGCCAGAA 1523					
DB 20 CCAAGGAGGAGGCCAGAA 1</					

Query Match	Best Local Similarity	1.2%; Score 20; DB 1; Length 20;	Indels	Gaps	0;
Matches 20; Conservative 0; Mismatches 0;					
QY 33 TCTCCACTCGGTCTGCTG 52					
DB 20 TCTCCACTCGGTCTGCTG 1					
RESULT 52					
AX546290/c					
LOCUS					
DEFINITION					
Sequence 39 from Patent EP1243290.					
AX546290					
ACCESSION					
VERSION					
KEYWORDS					
synthetic construct					
synthetic construct					
artificial sequences.					
ORGANISM					
REFERENCE					
1					
AUTHORS					
Besterman, J.M., Macleod, A.R. and Siders, W.M.					
TITLE					
Modulation of gene expression by combination therapy					
JOURNAL					
Patent: EP 1243290-A 39 25-SEP-2002;					
Methylgene, Inc. (CA)					
FEATURES					
source					
1..20					
Location/Qualifiers					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity					
1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 41 TCGTCACTCTGAGAACACA 60					
DB 20 TCGTCACTCTGAGAACACA 1					
RESULT 53					
AX546292/c					
LOCUS					
DEFINITION					
Sequence 41 from Patent EP1243290.					
AX546292					
ACCESSION					
VERSION					
KEYWORDS					
synthetic construct					
synthetic construct					
artificial sequences.					
ORGANISM					
REFERENCE					
1					
AUTHORS					
Besterman, J.M., Macleod, A.R. and Siders, W.M.					
TITLE					
Modulation of gene expression by combination therapy					
JOURNAL					
Patent: EP 1243290-A 41 25-SEP-2002;					
Methylgene, Inc. (CA)					
FEATURES					
source					
1..20					
Location/Qualifiers					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="oligonucleotide"					
Query Match					
Best Local Similarity					
1.2%; Score 20; DB 1; Length 20;					
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1504 CCAAGGAGGAGGAGCCAGAA 1523					
DB 20 CCAAGGAGGAGGAGCCAGAA 1					
RESULT 54					
AX546294/c					
LOCUS					
DEFINITION					
Sequence 43 from Patent EP1243290.					
AX546294					
ACCESSION					
VERSION					
KEYWORDS					
synthetic construct					
synthetic construct					
artificial sequences.					
ORGANISM					
REFERENCE					
1				</	

REFERENCE 1
 AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
 TITLE Modulation of gene expression by combination therapy
 JOURNAL Patent: EP 1243289-A 35 25-SEP-2002;
 Methylgene, Inc. (CA)

FEATURES
 source
 1..20 Location/Qualifiers

/organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

Query Match 1..2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCGCTGGTGGTGGTGGTCTC 36
 |||||
 Db 20 CCGCTGGTGGTGGTGGTCTC 1

RESULT 57
 AX546377/c
 LOCUS AX546377 20 bp DNA linear PAT 26-NOV-2002
 DEFINITION Sequence 36 from Patent EP1243289.
 ACCESSION AX546377
 VERSION AX546377.1 GI:25811568

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
 TITLE Modulation of gene expression by combination therapy
 JOURNAL Patent: EP 1243289-A 36 25-SEP-2002;
 Methylgene, Inc. (CA)

FEATURES
 source
 1..20 Location/Qualifiers

/organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

Query Match 1..2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GCTGTCTCCCACTCGGTCAT 48
 |||||
 Db 20 GCTGTCTCCCACTCGGTCAT 1

RESULT 58
 AX546378/c
 LOCUS AX546378 20 bp DNA linear PAT 26-NOV-2002
 DEFINITION Sequence 37 from Patent EP1243289.
 ACCESSION AX546378
 VERSION AX546378.1 GI:25811569

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
 TITLE Modulation of gene expression by combination therapy
 JOURNAL Patent: EP 1243289-A 37 25-SEP-2002;
 Methylgene, Inc. (CA)

FEATURES
 source
 1..20 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

Query Match 1..2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TGCTCTCCCACTCGGTCATCC 50
 |||||
 Db 20 TGCTCTCCCACTCGGTCATCC 1

RESULT 59
 AX546379/c
 LOCUS AX546379 20 bp DNA linear PAT 26-NOV-2002
 DEFINITION Sequence 38 from Patent EP1243289.
 ACCESSION AX546379
 VERSION AX546379.1 GI:25811570

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
 TITLE Modulation of gene expression by combination therapy
 JOURNAL Patent: EP 1243289-A 38 25-SEP-2002;
 Methylgene, Inc. (CA)

FEATURES
 source
 1..20 Location/Qualifiers

/organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

Query Match 1..2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 TCTCCCACTCGGTCATCCTG 52
 |||||
 Db 20 TCTCCCACTCGGTCATCCTG 1

RESULT 60
 AX546380/c
 LOCUS AX546380 20 bp DNA linear PAT 26-NOV-2002
 DEFINITION Sequence 39 from Patent EP1243289.
 ACCESSION AX546380
 VERSION AX546380.1 GI:25811571

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
 TITLE Modulation of gene expression by combination therapy
 JOURNAL Patent: EP 1243289-A 39 25-SEP-2002;
 Methylgene, Inc. (CA)

FEATURES
 source
 1..20 Location/Qualifiers

/organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

Query Match 1..2%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 TCGGTTCATCTCGAGAACACA 60
 |||||
 Db 20 TCGGTTCATCTCGAGAACACA 1

RESULT 61


```

Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1565 CCTCTCCAGCTCTGGCTTCC 1584
    |||||
Db 20 CCTCTCCAGCTCTGGCTTCC 1

RESULT 66
AX173370/c
LOCUS AX173370 24 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 24 from Patent WO0142445.
ACCESSION AX173370
VERSION AX173370.1 GI:114598145
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Murphy,B.R., Collins,P.L., Schmidt,A.C., Durbin,A.P.,
Skiaopoulos,M.H. and Tao,T.
TITLE Use of recombinant parainfluenza viruses (pivs) as vectors to
protect against infection and disease caused by piv and other human
pathogens
JOURNAL Patent: WO 0142445-A 24 14-JUN-2001;
The Secretary of the Department of Health and Human Services (US)
FEATURES
    source
        Location/Qualifiers
            1..24
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="HPV1 HN primer"

Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 633 ATTGATTTTCCATGTCGACGGC 656
    |||||
Db 24 ATTGCTATTTCCATGTCGACGGC 1

RESULT 67
BD244912/c
LOCUS BD244912 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244912
VERSION BD244912.1 GI:33054682
KEYWORDS JP 2002528391-A/40.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 40 03-SEP-2002;
METHYLGENE INC
COMMENT OS Artificial Sequence
PN JP 2002528391-A/40
PD 03-SEP-2002
PF 19-OCT-1999 JP 2000576885
PR 19-OCT-1998 US 50/104804
PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
706,
PC A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
09//
PC C12N5/10,C12N15/00,C12N5/00
CC antisense
FH Key Location/Qualifiers
FT source 1..20
    /organism="Artificial Sequence".

```

```

FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1531 GGGTCAAGGAGGAGGCCAAG 1550
    |||||
Db 20 GGGTCAAGGAGGAGGCCAAG 1

RESULT 68
AX546291/c
LOCUS AX546291 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 40 from Patent EP1243290.
ACCESSION AX546291
VERSION AX546291.1 GI:25811482
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 40 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="oligonucleotide"

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 62 CCTGAGCGCTCTGTCTACTC 81
    |||||
Db 20 CCTGAGCGCTCTGTCTACTC 1

RESULT 69
AX546293/c
LOCUS AX546293 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 42 from Patent EP1243290.
ACCESSION AX546293
VERSION AX546293.1 GI:25811484
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243290-A 42 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="oligonucleotide"

Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1531 GGGTCAAGGAGGAGGCCAAG 1550
    |||||

```

Db 20 GGGTCAAGGAGGAGGTCAAG 1
|||||
RESULT 70
AX546381/c
LOCUS AX546381 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 40 from Patent EP1243289.
ACCESSION AX546381
VERSION AX546381.1 GI:25811572
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
1 artificial sequences.
REFERENCE
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 42 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred.No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 62 CTTGAGCGCTCTCTGCACTC 81
|||||
Db 20 CTTGAGCGCTCTCTGCACTC 1
|||||
RESULT 71
AX546383/c
LOCUS AX546383 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 42 from Patent EP1243289.
ACCESSION AX546383
VERSION AX546383.1 GI:25811574
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: EP 1243289-A 42 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 1.1%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred.No. 42;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1531 GGGTCAAGGAGGAGGCAAG 1550
|||||
Db 20 GGGTCAAGGAGGAGGCAAG 1
|||||
RESULT 72
AX733295
LOCUS AX733295 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4929 from Patent WO03025175.
ACCESSION AX733295
VERSION AX733295.1 GI:30512638
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 4929 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 915 GATCGGTTAGGTGCTT 931
|||||
Db 1 GATCGGTTAGGTGCTT 17
|||||
RESULT 73
AX733529/c
LOCUS AX733529 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5163 from Patent WO03025175.
ACCESSION AX733529
VERSION AX733529.1 GI:30512872
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5163 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 902 CTCCTATCTGGGATC 918
|||||
Db 17 CTCCTATCTGGGATC 1
|||||
RESULT 74
BD244910/c
LOCUS BD244910 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Modulation of gene expression by combination therapy.
ACCESSION BD244910
VERSION BD244910.1 GI:33054680
KEYWORDS JP 2002528391-A/38.
SOURCE synthetic construct
ORGANISM synthetic construct
1 artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE Modulation of gene expression by combination therapy
JOURNAL Patent: JP 2002528391-A 38 03-SEP-2002;

[illegible]

RESULT 79
AR096054/c
LOCUS
DEFINITION Sequence 13 from patent US 6005087.
ACCESSION AR096054
VERSION AR096054.1 GI:10024506
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 6005087-A 13 21-DEC-1999;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
|||||
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 80
AR105513/c
LOCUS
DEFINITION Sequence 13 from patent US 6096720...
ACCESSION AR105513
VERSION AR105513.1 GI:12819110
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Love, W. Guy., Nicklin, P. Leslie., Hamilton, K. Ophelia. and Phillips, J. Ann.
TITLE Liposomal oligonucleotide compositions
JOURNAL Patent: US 6096720-A 13 01-AUG-2000;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
|||||
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 81
E49537/c
LOCUS
DEFINITION Antisense oligonucleotide regulation of raft gene expression.
ACCESSION E49537
VERSION E49537.1 GI:18628118
KEYWORDS JP 2000152797-A/27.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS P.M.B. and T.B.R.
TITLE Antisense oligonucleotide regulation of raft gene expression

JOURNAL Patent: JP 2000152797-A 27 06-JUN-2000;
COMMENT
OS ISIS PHARMACEUTICALS INC
PN Homo sapiens (human)
PD JP 2000152797-A/27
PF 06-JUN-2000
PR 18-JAN-2000 JP 2000008654
PI 31-MAY-1994 US 08/250856
PI MONIA BURETTO P BOGGUZO RUSSELL T
PC C12N15/09;A61K31/7088;A61K48/00;A61P17/06;A61P35/00;A61P43/00;
PC C12N15/00;A
CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Homo sapiens (human)"

FEATURES
source
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
|||||
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 82
I27257/c
LOCUS
DEFINITION Sequence 27 from patent US 5563255.
ACCESSION I27257
VERSION I27257.1 GI:1818033
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P. and Boggs, R.T.
TITLE Antisense oligonucleotide modulation of raf gene expression
JOURNAL Patent: US 5563255-A 27 08-OCT-1996;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1507 AGGAGGAGAGCCAGAG 1524
|||||
Db 19 AGGAGGAGAGCCAGCAG 2

RESULT 83
AR212287/c
LOCUS
DEFINITION Sequence 13 from patent US 6399754.
ACCESSION AR212287
VERSION AR212287.1 GI:21515821
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook, P. Dan.
TITLE Sugar modified oligonucleotides
JOURNAL Patent: US 6399754-A 13 04-JUN-2002;
FEATURES
source
Location/Qualifiers
1..20

```

/organism="unknown"
/mol_type="unassigned DNA"

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1507 AGGAGGAGAGCCGAGAG 1524
Db 19 AGGAGGAGAGCCGAGCAG 2

RESULT 84
LOCUS AR215981/c
DEFINITION Sequence 28 from patent US 6410518.
ACCESSION AR215981
VERSION AR215981.1 GI:23314269
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P.
TITLE Antisense oligonucleotide inhibition of raf gene expression
JOURNAL Patent: US 6410518-A 28 25-JUN-2002;
FEATURES
    source
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1507 AGGAGGAGAGCCGAGAG 1524
Db 19 AGGAGGAGAGCCGAGCAG 2

RESULT 85
LOCUS AR231421/c
DEFINITION Sequence 13 from patent US 6451991.
ACCESSION AR231421
VERSION AR231421.1 GI:27272504
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Martin,P., Altmann,K.-H., Cook,P.D. and Monia,B.P.
TITLE Sugar-modified gapped oligonucleotides
JOURNAL Patent: US 6451991-A 13 17-SEP-2002;
FEATURES
    source
        1..20
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1507 AGGAGGAGAGCCGAGAG 1524
Db 19 AGGAGGAGAGCCGAGCAG 2

RESULT 86
LOCUS BD255496/c
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255496

```

```

VERSION BD255496.1 GI:33065266
KEYWORDS JF:20Q2541795-A/3289.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 20Q2541795-A 3289 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 20Q2541795-A/3289
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91), C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source 1..17
FT /organism="Eukaryote".
FT Location/Qualifiers
    1..17
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1417 ACTTCARAAAGCCCAAG 1433
Db 17 ACTTCARAAAGCCCAAG 1

RESULT 87
LOCUS BD255497/c
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255497
VERSION BD255497.1 GI:33065267
KEYWORDS JF:20Q2541795-A/3290.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 20Q2541795-A 3290 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 20Q2541795-A/3290
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91), C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH

```

```
Key      Location/Qualifiers
FT       source
          1..17
          /organism="Eukaryote".
FEATURES
  source
    1..17
    Location/Qualifiers
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1415 CAACCTCAAAAGGCCA 1431
Db 17 CAACCTCAAAATAGGCCA 1
RESULT 88
LOCUS AR293317 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5052 from patent US 6537751.
ACCESSION AR293317
VERSION AR293317.1 GI:31680601
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 18)
  Cohen, D., Chumakov, I. and Blumenfeld, M.
  Biallelic markers for use in constructing a high density
  disequilibrium map of the human genome
  Patent: US 6537751-A 5052 25-MAR-2003;
  Location/Qualifiers
  source
    1..18
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1469 ACAGGAGAGAGAGGAA 1485
Db 17 ACAGGAGAGAGATGGAA 1
RESULT 89
LOCUS AR035154 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5871730.
ACCESSION AR035154
VERSION AR035154.1 GI:5951822
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 18)
  Brzezinski, R., Dery, C.V. and Beaulieu, C.
  Thermostable xylanase DNA, protein and methods of use
  Patent: US 5871730-A 14 16-FEB-1999;
  Location/Qualifiers
  source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 689 CATGACTGCTGCTTCA 706
Db 18 CATGGCTGCTGCTTCA 1
Key      Location/Qualifiers
FT       source
          1..17
          /organism="Eukaryote".
FEATURES
  source
    1..17
    Location/Qualifiers
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
Query Match      1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1415 CAACCTCAAAAGGCCA 1431
Db 17 CAACCTCAAAATAGGCCA 1
RESULT 88
LOCUS AR293317 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5052 from patent US 6537751.
ACCESSION AR293317
VERSION AR293317.1 GI:31680601
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 18)
  Cohen, D., Chumakov, I. and Blumenfeld, M.
  Biallelic markers for use in constructing a high density
  disequilibrium map of the human genome
  Patent: US 6537751-A 5052 25-MAR-2003;
  Location/Qualifiers
  source
    1..18
    /organism="unknown"
    /mol_type="genomic DNA"
Query Match      1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1469 ACAGGAGAGAGAGGAA 1485
Db 17 ACAGGAGAGAGATGGAA 1
RESULT 89
LOCUS AR035154 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5871730.
ACCESSION AR035154
VERSION AR035154.1 GI:5951822
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 18)
  Brzezinski, R., Dery, C.V. and Beaulieu, C.
  Thermostable xylanase DNA, protein and methods of use
  Patent: US 5871730-A 14 16-FEB-1999;
  Location/Qualifiers
  source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 689 CATGACTGCTGCTTCA 706
Db 18 CATGGCTGCTGCTTCA 1
RESULT 90
LOCUS AR127642 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 60 from patent US 6180774.
ACCESSION AR127642
VERSION AR127642.1 GI:14114237
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 18)
  Brown, S. Marie., Dean, D. Allen., Fromm, M. Ernest. and
  Sanders, P. Rigden.
  Synthetic DNA sequences having enhanced expression in
  monocotyledonous plants and method for preparation thereof
  Patent: US 6180774-A 60 30-JAN-2001;
  Location/Qualifiers
  source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 646 ATGGTCACGGCGGTGGAAG 663
Db 18 ATGGTCGCGGCGTCTGAAG 1
RESULT 91
LOCUS AR174568 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 23 from patent US 6307024.
ACCESSION AR174568
VERSION AR174568.1 GI:17914888
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 18)
  Novak, J. E., Presnell, S. R., Sprecher, C. A., Foster, D. C., Holly, R. D.,
  Gross, J. A., Johnston, J. V., Nelson, S. R. and
  Hammond, A. K.
  Cytokine zalphall Ligand
  Patent: US 6307024-A 23 23-OCT-2001;
  Location/Qualifiers
  source
    1..18
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match      0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 511 ATTCGGCTGGGGGCTGTC 528
Db 1 ACTGGCTGGGGGACTGTC 18
RESULT 92
LOCUS BD237586 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Cytokine receptor ZALPHALL.
ACCESSION BD237586
VERSION BD237586.1 GI:33047356
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 18)
  JP 2002526062-A/20.
  synthetic construct
  artificial sequences.
```

Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.

AUTHORS
TITLE
JOURNAL

Patent: JP 2002526062-A 20 20-AUG-2002;

ZYMOGENETICS INC

OS Artificial Sequence

PN JP 2002526062-A/20

PD 20-AUG-2002

PF 23-SEP-1999 JP 2000574143

PR 23-SEP-1998 US 09/159254,09-MAR-1999 US 09/265117 PR

PI SCOTT R PRESNELL, DARRELL C CONKLIN, JULIA E NOVAK, ANGELA K PI

PC C12N15/09, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC

PC C12N5/10

PC C12P21/02, C12P21/08, C12Q1/04, G01N33/53, G01N33/566, C12N15/00,

PC C12N5/00

CC Oligonucleotide primer ZC19954

CC Key Location/Qualifiers

FT source 1.18

FT /organism='Artificial Sequence'

FT Location/Qualifiers

1.18

/organism='synthetic construct'

/mol_type='genomic DNA'

/db_xref='taxon:32630'

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528

Db 1 ACTGGGCTGGGGACTGC 18

RESULT 93

BD237603

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.

Cytokine receptor ZALPHA11

Patent: JP 2002526062-A 37 20-AUG-2002;

ZYMOGENETICS INC

OS Artificial Sequence

PN JP 2002526062-A/37

PD 20-AUG-2002

PF 23-SEP-1999 JP 2000574143

PR 23-SEP-1998 US 09/159254,09-MAR-1999 US 09/265117 PR

PI SCOTT R PRESNELL, DARRELL C CONKLIN, JULIA E NOVAK, ANGELA K PI

PC C12N15/09, C07K14/715, C07K16/28, C12N1/15, C12N1/19, C12N1/21, PC

PC C12N5/10,

PC C12P21/02, C12P21/08, C12Q1/04, G01N33/53, G01N33/566, C12N15/00,

PC C12N5/00

CC Oligonucleotide primer ZC19954

CC Key Location/Qualifiers

FT source 1.18

FT /organism='Artificial Sequence'

FT Location/Qualifiers

1.18

/organism='synthetic construct'

/mol_type='genomic DNA'

/db_xref='taxon:32630'

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528

Db 1 ACTGGGCTGGGGACTGC 18

RESULT 93

BD237603

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.

Cytokine receptor ZALPHA11

Patent: JP 2002526062-A 37 20-AUG-2002;

ZYMOGENETICS INC

OS Artificial Sequence

Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528

Db 1 ACTGGGCTGGGGACTGC 18

RESULT 94

BD248961

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Novak,J.E., Presnell,S.R., Sprechter,C.A., Foster,D.C., Holly,R.D.,

Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and

Hammond,A.K.

Novel cytokine ZALPHA11 ligand

Patent: JP 2002537839-A 24 12-NOV-2002;

ZYMOGENETICS INC

OS Artificial Sequence

PN JP 2002537839-A/22

PD 12-NOV-2002

PF 09-MAR-2000 JP 2000603382

PR 09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR

PI JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPRECHTER, DONALD C PI

PC C12N15/09, C07K14/53, C07K14/55, C07K16/24, C07K19/00, C12N1/15, C12N1/19, PC

PC C07K14/54, C07K14/55, C07K16/24, C07K19/00, C12N1/15, C12N1/19, PC

PC C12N5/10, C12P21/02, C12P21/02, G01N33/53, C12N15/00, C12N5/00, PC

PC A61K37/02

CC Oligonucleotide primer ZC19954

CC Key Location/Qualifiers

FT source 1.18

FT /organism='Artificial Sequence'

FT Location/Qualifiers

1.18

/organism='synthetic construct'

/mol_type='genomic DNA'

/db_xref='taxon:32630'

Query Match

Best Local Similarity 88.9%; Pred. No. 87;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATTGGGCTGGGGCCTGC 528

Db 1 ACTGGGCTGGGGACTGC 18

RESULT 95

I75311/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Sequence 60 from patent US 5689052.

I75311

I75311

I75311.1

GI:3011452

Unknown.

Unclassified.

1 (bases 1 to 18)

Brown,S.Marie., Dean,D.Allen., Fromm,M.Ernest. and

Sanders,P.Rigden.

TITLE Synthetic DNA sequences having enhanced expression in monocotyledonous plants and method for preparation thereof
JOURNAL Patent: US 5689052-A 60 18-NOV-1997;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 646 ATGTTGACGGGTGAAG 663
Db 18 ATGTTGCGGGCTCGAAG 1

RESULT 96
AR342894
LOCUS 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 22 from patent US 6576744.
ACCESSION AR342894
VERSION AR342894.1 GI:33738193
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor zalphall
JOURNAL Patent: US 6576744-A 22 10-JUN-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATGGGCTGGGGCCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 97
AR342911
LOCUS 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 39 from patent US 6576744.
ACCESSION AR342911
VERSION AR342911.1 GI:33738210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Presnell,S.R., Conklin,D.C., Novak,J.E. and Hammond,A.K.
TITLE Cytokine receptor zalphall
JOURNAL Patent: US 6576744-A 39 10-JUN-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATGGGCTGGGGCCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 98
AR374060
LOCUS 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6605272.
ACCESSION AR374060
VERSION AR374060.1 GI:40076632
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Methods of using zalphall ligand
JOURNAL Patent: US 6605272-A 23 12-AUG-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 511 ATGGGCTGGGGCCCTGC 528
Db 1 ACTGGGCTGGGGGACTGC 18

RESULT 99
AR374065
LOCUS 18 bp DNA linear PLN 23-OCT-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 454G11.
ACCESSION AJ597665
VERSION AJ597665.1 GI:37947293
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE 1
AUTHORS Brunaud V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepoint,L., Caboche,N. and Leclercq,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 18)
AUTHORS Balzerque,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the a corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbioigen.fr>).

FEATURES Location/Qualifiers
source 1..18
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"

misc_feature

/db_xref="taxon:3702"
/clone="454G11"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1..18
/note="T-DNA flanking sequence
left border"

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 593 GGAAGTCTAAAGTATCA 610
|||||
Db 1 GGAAGTCTAAAGTATCA 18

RESULT 100
BD231175/c
LOCUS BD231175 16 bp DNA linear PAT 17-JUL-2003
DEFINITION Antagonist based on receptor and prepration and utilization methods.
ACCESSION BD231175
VERSION BD231175.1 GI:33040945
KEYWORDS JP 2002525119-A/1.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 16)
AUTHORS Stahl,N. and Yancopoulos,G.D.
TITLE Antagonist based on receptor and prepration and utilization methods
JOURNAL Patent: JP 2002525119-A 1 13-AUG-2002;
COMMENT REGENERON PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002525119-A/1
PD 13-AUG-2002
PF 22-SEP-1999 JP 2000572379
PR 25-SEP-1998 US 60/101858,19-MAY-1999 US 09/313942 PI
PC C12N15/09,C07K14/715,C07K19/00,C12N1/19,C12N1/21,C12N5/10, PC
C12P21/02//
PC A61K39/00,A61P19/10,A61P35/00,(C12P21/02,C12R1/91),C12N15/00,
PC C12N5/00,
PC A61K37/02
CC Kozak sequence Location/Qualifiers
FH Key 1..16
FT source
FT Location/Qualifiers
1..16
/organism="Artificial Sequence".

FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGCTGACGGCG 657
|||||
Db 16 CACCATGCTGACGGCG 1

RESULT 101
AR242277/c
LOCUS AR242277 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6472179.
ACCESSION AR242277
VERSION AR242277.1 GI:27288127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)

AUTHORS Stahl,N. and Yancopoulos,G.D.
TITLE Receptor based antagonists and methods of making and using
JOURNAL Patent: US 6472179-A 3 29-OCT-2002;
FEATURES Location/Qualifiers
1..16
source
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 642 CACCATGCTGACGGCG 657
|||||
Db 16 CACCATGCTGACGGCG 1

RESULT 102
AR328425
LOCUS AR328425 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5827 from patent US 6566127.
ACCESSION AR328425
VERSION AR328425.1 GI:33714233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5827 20-MAY-2003;
FEATURES Location/Qualifiers
1..16
source
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCTGCACCA 532
|||||
Db 1 CTGGGGGCTGCACCA 16

RESULT 103
AX503577/c
LOCUS AX503577 16 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 3 from Patent EP1229047.
ACCESSION AX503577
VERSION AX503577.1 GI:23385865
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE artificial sequences.
1
AUTHORS Yancopoulos,G.D. and Stahl,N.
TITLE Il-1 receptor fusion proteins used as antagonists and methods of making and using
JOURNAL Patent: EP 1229047-A 3 07-AUG-2002;
FEATURES REGENERON PHARMACEUTICALS, INC. (US)
1..16
source
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Kozak sequence"

Query Match 0.9%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 642 CACCATGGTGCGCG 657
Db 16 CACCATGGTGCGCG 1

RESULT 104
BD255495/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255495
VERSION BD255495.1 GI:33065265
KEYWORDS JP 2002541795-A/3288.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3288 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/3288
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1..17
FT Location/Qualifiers
    source
        /organism='Eukaryote'.
        /organism='unidentified'
        /mol_type='genomic DNA'
        /db_xref='taxon:32644'

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1415 CAATTTCAAAAGCC 1430
Db 16 CAATTTCAAAAGCC 1

RESULT 106
LOCUS
DEFINITION Sequence 4754 from patent US 6566127.
ACCESSION AR327352
VERSION AR327352.1 GI:33713160
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4754 20-MAY-2003;
FEATURES
    source
        /organism='unknown'
        /mol_type='unassigned RNA'

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 517 CTGGGGGCGCTGCACCA 532
Db 1 CTGGGGGCGCTGCACCA 16

RESULT 107
LOCUS
DEFINITION Sequence 3088 from Patent WO0159103.
ACCESSION AX217646
VERSION AX217646.1 GI:15527707
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
ncgo gene expression
JOURNAL Patent: WO 0159103-A 3088 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

QY 1418 CTTCAAAAAGCCCAAG 1433
Db 17 CTTCAAAAAGCCCAAG 2

RESULT 105
BD255498/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255498
VERSION BD255498.1 GI:33065268
KEYWORDS JP 2002541795-A/3291.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3291 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/3291
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390

```


FEATURES		McSwiggen, James (US) ; Chowrira, Bharat M. (US)		Best Local Similarity 93.8%; Pred. No. 86;		Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
source		1. 17		Location/Qualifiers			
		/organism="synthetic construct"					
		/mol_type="unassigned RNA"					
		/db_xref="taxon:32630"					
		/note="Nucleic Acid"					
Query Match		0.9%; Score 14.4; DB 1; Length 17;					
Best Local Similarity		93.8%; Pred. No. 86;					
Matches		15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY		1119 TTGGACCAAGATTCA 1134					
DB		17 TTGGACCAAGATTGCA 2					
RESULT 108							
AX218225/c							
LOCUS		AX218225		17 bp RNA		linear PAT 07-SEP-2001	
DEFINITION		Sequence 3667 from Patent WO0159103.					
ACCESSION		AX218225					
VERSION		AX218225.1 GI:15528286					
KEYWORDS		synthetic construct					
SOURCE		synthetic construct					
ORGANISM		artificial sequences.					
REFERENCE		1					
AUTHORS		Blatt, L., McSwiggen, J. and Chowrira, B.M.					
TITLE		Method and reagent for the modulation and diagnosis of cd20 and					
JOURNAL		nogo gene expression					
		Patent: WO 0159103-A 3667 16-AUG-2001;					
		RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;					
		McSwiggen, James (US) ; Chowrira, Bharat M. (US)					
FEATURES		Location/Qualifiers					
source		1. 17					
		/organism="synthetic construct"					
		/mol_type="unassigned RNA"					
		/db_xref="taxon:32630"					
		/note="Nucleic Acid"					
Query Match		0.9%; Score 14.4; DB 1; Length 17;					
Best Local Similarity		93.8%; Pred. No. 86;					
Matches		15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY		1119 TTGGACCAAGATTCA 1134					
DB		16 TTGGACCAAGATTGCA 1					
RESULT 109							
AX475558/c							
LOCUS		AX475558		17 bp DNA		linear PAT 12-AUG-2002	
DEFINITION		Sequence 779 from Patent WO0224750.					
ACCESSION		AX475558					
VERSION		AX475558.1 GI:22214843					
KEYWORDS		Homo sapiens (human)					
SOURCE		Homo sapiens					
ORGANISM		Homo sapiens					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE		1					
AUTHORS		Zhang, J.					
TITLE		Human kidney tumor overexpressed membrane protein 1					
JOURNAL		Patent: WO 0224750-A 779 28-MAR-2002;					
		Aeomica, Inc. (US)					
FEATURES		Location/Qualifiers					
source		1. 17					
		/organism="Homo sapiens"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
Query Match		0.9%; Score 14.4; DB 1; Length 17;					
Best Local Similarity		93.8%; Pred. No. 86;					
Matches		15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY		1247 CCAAACGACGCGGATT 1262					
DB		16 CCAAATGACGCGGATT 1					
RESULT 111							
AX784017/c							
LOCUS		AX784017		17 bp DNA		linear PAT 17-JUL-2003	
DEFINITION		Sequence 2348 from Patent WO03050284.					
ACCESSION		AX784017					
VERSION		AX784017.1 GI:32951866					
KEYWORDS		Homo sapiens (human)					
SOURCE		Homo sapiens					
ORGANISM		Homo sapiens					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE		1					
AUTHORS		Guo, J.					
TITLE		Human prostate cancer candidate protein 1					
JOURNAL		Patent: WO 03050284-A 2348 19-JUN-2003;					
		Amersham Biosciences (SV) Corp. (US)					
FEATURES		Location/Qualifiers					
source		1. 17					
		/organism="Homo sapiens"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
Query Match		0.9%; Score 14.4; DB 1; Length 17;					
Best Local Similarity		93.8%; Pred. No. 86;					
Matches		15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY		1501 AAACCAAGGAGGAGAA 1516					
DB		17 AAACCAAGGAGGAGCA 2					
RESULT 112							
AX784018/c							
LOCUS		AX784018		17 bp DNA		linear PAT 17-JUL-2003	

```
DEFINITION Sequence 2349 from Patent WO03050284.
ACCESSION AX784018
VERSION AX784018.1 GI:32951867
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2349 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1501 AAACCAAGGAGGAGAA 1516
16 AAACCAAGGAGGAGCA 1
Db

RESULT 113
AR267656 18 bp DNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 46 from patent US 6497880.
ACCESSION AR267656
VERSION AR267656.1 GI:29697764
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wisniewski, J.
TITLE Heat shock genes and proteins from Neisseria meningitidis, Candida
glabrata and Aspergillus fumigatus
JOURNAL Patent: US 6497880-A 46 24-DEC-2002;
FEATURES
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 AGCCCAATCCTGAGGA 298
2 AGCCCAATCCGAGGA 17
Db

RESULT 114
AR292367 18 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 4102 from patent US 6537751.
ACCESSION AR292367
VERSION AR292367.1 GI:31679651
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4102 25-MAR-2003;
FEATURES
source
1..18
/organism="synthetic construct"
```

```
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCTCGGGTCTCTG 16
|||||
Db 1 ATGCTCGGTGTCTCTG 16
|||||

RESULT 115
AR297444 18 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 9179 from patent US 6537751.
ACCESSION AR297444
VERSION AR297444.1 GI:31684728
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9179 25-MAR-2003;
FEATURES
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1457 AGAGAAAGACCCAGAG 1472
|||||
Db 1 AGAGAAAGAACCCAGAG 15
|||||

RESULT 116
BD057516/c 18 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Cytochrome 7 receptor.
ACCESSION BD057516
VERSION BD057516.1 GI:22603122
KEYWORDS JP 2001514493-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lok, S., Kho, C. J., Jelmsberg, A. C., Adams, R. L., Whitmore, T. E. and
Farrah, T. M.
TITLE Cytochrome 7 receptor
JOURNAL Patent: JP 2001514493-A 3 11-SEP-2001;
ZymoGenetics Inc
COMMENT PN JP 2001514493-A/3
PD 11-SEP-2001
PF 18-FEB-1998 JP 1998536782
PR 20-FEB-1997 US 08/803305, 02-OCT-1997 US 08/943087 PI
SI LOK, CHOON J KHO, ANNA C JELMSBERG, ROBYN L ADAMS, THEODORE E PI
WHITMORE,
PI THERESA M FARRAH
PC C12N15/12, C07K14/715, C12N15/62, C07K16/28, C07K16/42, C07K19/00,
PC G01N33/50
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FEATURES
source
1..18
/organism="synthetic construct"
```

Db	15	AAACCAAGGAGGAG 2
RESULT 119	AX784020	17 bp DNA linear PAT 17-JUL-2003
LOCUS	AX784020/c	
DEFINITION	Sequence 2351 from Patent WO03050284.	
ACCESSION	AX784020	
VERSION	AX784020.1	GI:32951869
KEYWORDS	Human prostate cancer candidate protein 1	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Guo, J.	
AUTHORS	Human prostate cancer candidate protein 1	
TITLE	Patent: WO 03050284-A 2351 19-JUN-2003;	
JOURNAL	Amersham Biosciences (SV) Corp. (US)	
FEATURES	Location/Qualifiers	
source	1..17	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
Query Match	0.9%; Score 14; DB 1; Length 17;	
Best Local Similarity	100.0%; Pred. No. 95; 0; Indels 0; Gaps 0;	
Matches	14; Conservative 0; Mismatches 0;	
QY	1501 AAACCAAGGAGGAG 1514	
Db	14 AAACCAAGGAGGAG 1	
RESULT 120	AL2195	17 bp DNA linear PAT 10-DEC-1993
LOCUS	AL2195	
DEFINITION	EBI 782.	
ACCESSION	AL2195	
VERSION	AL2195.1	GI:491298
KEYWORDS	synthetic construct	
SOURCE	synthetic construct	
ORGANISM	artificial sequences.	
REFERENCE	1 (bases 1 to 17)	
AUTHORS	Heckl, K., Spevak, W., Ostermann, E., Zoepfel, A., Krystek, E., Maurer-Fogy, I., Wiche-Castanon, M.J., Stratowa, C. and Hauptmann, R.	
TITLE	Human manganese superoxide dismutase (Mn-SOD)	
JOURNAL	Patent: EP 0282899-A 18 21-SEP-1988;	
FEATURES	BOEHRINGER INGELHEIM INTERNATIONAL GmbH	
source	Location/Qualifiers	
	1..17	
	/organism="synthetic construct"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:32630"	
Query Match	0.9%; Score 13.8; DB 1; Length 17;	
Best Local Similarity	88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;	
Matches	15; Conservative 0; Mismatches 2;	
QY	857 GGAGATGTTCCAGCCCTA 873	
Db	1 GGAGATGTTACAGCCCA 17	
RESULT 121	AL26903	17 bp DNA linear PAT 05-JUN-1995
LOCUS	AL26903	
DEFINITION	Primer 10.	
ACCESSION	A26903	
VERSION	A26903.1	GI:1248331
KEYWORDS	synthetic construct	
SOURCE	synthetic construct	

```
ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS 1 (bases 1 to 17)
TITLE IMPROVEMENTS IN OLIGONUCLEOTIDE PRIMERS AND PROBES
JOURNAL Patent: WO 9305176-A 19 18-MAR-1993;
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 CAAGGAGGAGGCGCAAGT 1551
Db 17 CAAAAGGAGGCGCAAGT 1

RESULT 122
LOCUS AR158444 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 66 from patent US 6251588.
ACCESSION AR158444
VERSION AR158444.1 GI:16220483
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 66 26-JUN-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTGGGCTCTGCCCC 19
Db 17 GTCTGGGCTCTGCCCC 1

RESULT 123
BD254323/c
LOCUS BD254323 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254323
VERSION BD254323.1 GI:33064093
KEYWORDS JP 2002541795-A/2116.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and McSwiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2116 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2116
PD 10-DEC-2002
PR 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N5/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,

ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS 1 (bases 1 to 17)
TITLE IMPROVEMENTS IN OLIGONUCLEOTIDE PRIMERS AND PROBES
JOURNAL Patent: WO 9305176-A 19 18-MAR-1993;
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 CAAGGAGGAGGCGCAAGT 1551
Db 17 CAAAAGGAGGCGCAAGT 1

RESULT 122
LOCUS AR158444 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 66 from patent US 6251588.
ACCESSION AR158444
VERSION AR158444.1 GI:16220483
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 66 26-JUN-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTGGGCTCTGCCCC 19
Db 17 GTCTGGGCTCTGCCCC 1

RESULT 123
BD254323/c
LOCUS BD254323 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254323
VERSION BD254323.1 GI:33064093
KEYWORDS JP 2002541795-A/2116.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and McSwiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2116 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2116
PD 10-DEC-2002
PR 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N5/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,

PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N5/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source 1..17
/organism="Eukaryote".
FT Location/Qualifiers
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 CCTGAGAACACAGCCTG 65
Db 17 CCTGAGAACACAGCCTG 1

RESULT 124
LOCUS AR186914 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2402 from patent US 6346398.
ACCESSION AR186914
VERSION AR186914.1 GI:20232879
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2402 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGCTGTGAAACTT 482
Db 1 CAAGTGCTGTGAAACTT 17

RESULT 125
AR190268/c
LOCUS AR190268 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5756 from patent US 6346398.
ACCESSION AR190268
VERSION AR190268.1 GI:20236233
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5756 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
```

```
Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGGTGTGCTGTC 34
Db 17 CTGCTGGTGTGCTGTC 1

RESULT 126
LOCUS AR195652 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 117 from patent US 6350934.
ACCESSION AR195652
VERSION AR195652.1 GI:20245089
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P,Ann.Owens.,
TITLE Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
JOURNAL Nucleic acid encoding delta-9 desaturase
PATENT Patent: US 6350934-A 117 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 495 ACGACATCGCCGTGAA 511
Db 1 AAGTACATCGCCGTGAA 17

RESULT 127
LOCUS AR323545 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 947 from patent US 6566127.
ACCESSION AR323545
VERSION AR323545.1 GI:33709353
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 947 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 466 CAAGTGTCTGAACTT 482
Db 1 CAAGTGTCTGAACTT 17

RESULT 128
LOCUS AR325233/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2635 from patent US 6566127.
ACCESSION AR325233
```

```
VERSION AR325233.1 GI:33711041
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 8535 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 CCGCTGGTGTGCTGTC 34
Db 17 CTGCTGGTGTGCTGTC 1

RESULT 129
LOCUS AR327353 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4755 from patent US 6566127.
ACCESSION AR327353
VERSION AR327353.1 GI:33713161
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4755 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 518 TGGGGGCGCTGCACCATG 534
Db 1 TGGGAGCCCTGCACCAAG 17

RESULT 130
LOCUS AR327354 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4756 from patent US 6566127.
ACCESSION AR327354
VERSION AR327354.1 GI:33713162
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4756 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
```

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 521 GGGCTGCACCATCAA 537
1 GAGCTGCACCAAGCAA 17

Db

RESULT 131
LOCUS AR327355 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4757 from patent US 6566127.
ACCESSION AR327355
VERSION AR327355.1 GI:33713163
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4757 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 523 GCCTGCACCATGCAAG 539
1 GCCTGCACCAAGCAAG 17

Db

RESULT 132
LOCUS AR327356 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4758 from patent US 6566127.
ACCESSION AR327356
VERSION AR327356.1 GI:33713164
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4758 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 CCTGCACCATGCAAGA 540
1 CCTGCACCAAGCAAGA 17

Db

RESULT 133
LOCUS AR327992/c 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5394 from patent US 6566127.
ACCESSION AR327992
VERSION AR327992.1 GI:33713800

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5394 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 396 GTTGTGAGGACTGTCC 412
17 GTTGTGAGGACTGTCC 1

Db

RESULT 134
LOCUS AR363927 17 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 22 from patent US 5240847.
ACCESSION AR363927
VERSION AR363927.1 GI:34426034
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Heckl,K., Spevak,M., Ostermann,E., Zophel,A., Krystek,E., Maurer-Fogy,I., Wiche-Castanon,M.J., Stratowa,C. and Hauptmann,R.
TITLE Human manganese superoxide dismutase (hMn-SOD)
JOURNAL Patent: US 5240847-A 22 31-AUG-1993;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 857 GGAGATGTTCCAGCCTA 873
1 GGAGATGTTACAGCCCA 17

Db

RESULT 135
LOCUS AX037535/c 17 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 160 from Patent WO0056922.
ACCESSION AX037535
VERSION AX037535.1 GI:11226962
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Norberg,L.T., Olaisson,E., Jonsson,L., Lindstrom,P.H. and Sanders,R.
TITLE Genetic polymorphism and polymorphic pattern for assessing disease status, and compositions for use thereof
JOURNAL Patent: WO 0056922-A 160 28-SEP-2000;
NORBERG LEIF TORBJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE) ; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ; SANDERS RHIANNON (SE)
FEATURES Location/Qualifiers
source 1..17

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTCGCGCCGCTGGTCT 28
Db 17 CTGCGCCGCTGGTCT 1

RESULT 136
LOCUS AX272526 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 95 from Patent WO0162911.
ACCESSION AX272526
VERSION AX272526.1 GI:16545263
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 95 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1562 GGACTCTCCAGCTGTG 1578
Db 1 GGACTCTCCATCTGT 17

RESULT 137
LOCUS AX422324 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 660 from Patent WO0188124.
ACCESSION AX422324
VERSION AX422324.1 GI:21525706
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 660 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 298 AGATGACCAAGTACCAC 314
Db 1 AGATGACCAAGGACGAC 17

RESULT 138
LOCUS AX422476 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 812 from Patent WO0188124.
ACCESSION AX422476
VERSION AX422476.1 GI:21525858
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 812 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 142 TCTGTACTACTACGAC 158
Db 1 TCGGTACTACTATGAC 17

RESULT 139
LOCUS AX475000 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 221 from Patent WO0224750.
ACCESSION AX475000
VERSION AX475000.1 GI:22214285
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 221 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1583 CCTGCTGACTCCCTCAC 1599
Db 1 CCTGCTGACTCCACAC 17

RESULT 140
LOCUS AX499281 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 588 from Patent EP1229046.
ACCESSION AX499281

```

VERSION      AX499281.1  GI:23381574
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      Zhan, J.
TITLE        Human testis expressed patched like protein
JOURNAL      Patent: EP 1229046-A 588 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES     source
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1456 AAGAGAGAGCCAGGAG 1472
Db 1 AAGAGAGAGCCCTAGAG 17

RESULT 141
AX499282
LOCUS       AX499282               17 bp  DNA  linear  PAT 27-SEP-2002
DEFINITION Sequence 589 from Patent EP1229046.
ACCESSION  AX499282
VERSION     AX499282.1  GI:23381575
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 589 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES    source
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1457 AGAGAGAGCCAGGAG 1473
Db 1 AGAGAGAGCCCTAGAG 17

RESULT 142
AX499283
LOCUS       AX499283               17 bp  DNA  linear  PAT 27-SEP-2002
DEFINITION Sequence 590 from Patent EP1229046.
ACCESSION  AX499283
VERSION     AX499283.1  GI:23381576
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 590 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES     source
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1458 GAGAGAGCCAGGAG 1474
Db 1 GAGAGAGCCCTAGAG 17

RESULT 143
AX499284
LOCUS       AX499284               17 bp  DNA  linear  PAT 27-SEP-2002
DEFINITION Sequence 591 from Patent EP1229046.
ACCESSION  AX499284
VERSION     AX499284.1  GI:23381577
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 591 07-AUG-2002;
             Aeomica, Inc. (US)
FEATURES    source
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1459 AGAAGAGCCAGGAG 1475
Db 1 AGGAGAGCCCTAGAG 17

RESULT 144
AX578270/c
LOCUS       AX578270/c             17 bp  RNA  linear  PAT 10-JAN-2003
DEFINITION Sequence 108 from Patent WO0211674.
ACCESSION  AX578270
VERSION     AX578270.1  GI:27647472
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Symkowski, D.E.
             and Grupe, A.
TITLE       Method and reagent for the inhibition of calcium activated chloride
             channel-1 (Clca-1)
JOURNAL     Patent: WO 0211674-A 108 14-FEB-2002;
             RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
             Thompson, James (US)
FEATURES     source
             1..17
             /organism="Homo sapiens"
             /mol_type="unassigned RNA"
             /db_xref="taxon:9606"

Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;

```



```

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 374 CAACAGATCAGAGAT 390
Db 17 CAACAGATCAGAGAT 1

RESULT 145
AX601040/c
LOCUS AX601040 17 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 135 from Patent WO02092851.
ACCESSION AX601040
VERSION AX601040.1 GI:28401113
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM Binns,M.M. and Swinburne,J.E.
REFERENCE 1
AUTHORS Binns,M.M. and Swinburne,J.E.
TITLE Genetic typing
JOURNAL Patent: WO 02092851-A 135 21-NOV-2002;
ANIMAL HEALTH TRUST (GB); The British Horseracing Board (GB)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="synthetic DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 GTGCTGCTGCTCCAC 40
Db 17 GTCCTGCTGCTCCAC 1

RESULT 146
AX649489/c
LOCUS AX649489 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1329 from Patent EP1273660.
ACCESSION AX649489
VERSION AX649489.1 GI:29152307
KEYWORDS Human sodium-hydrogen exchanger like protein 1
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,X.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1329 08-JAN-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1381 AAGAGGAGGAGAGGGG 1397
Db 17 AGGAGGAGGAGAGGGG 1

RESULT 147
AX722800/c
LOCUS AX722800 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 487 from Patent WO03025176.

```

```

ACCESSION AX722800
VERSION AX722800.1 GI:30423301
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 487 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 30 CTGCTCCGACTCGGTC 46
Db 17 CTGCTCCGACTCGATC 1

RESULT 148
AX727998
LOCUS AX727998 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5685 from Patent WO03025176.
ACCESSION AX727998
VERSION AX727998.1 GI:30507341
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5685 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1328 GATCTCTCTCTTGACA 1344
Db 1 GATCTCTCTATTGACA 17

RESULT 149
AX735917
LOCUS AX735917 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1507 from Patent WO03025177.
ACCESSION AX735917
VERSION AX735917.1 GI:30515194
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

FEATURES	source	Location/Qualifiers
Query Match		0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity		88.2%; Pred. No. 1e+02;
Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1573	GCTCTGGCTTCTGCTG 1589
DB	1	GATCTGCTTCTGCTG 17
RESULT 152		
AX759597/C		17 bp DNA linear PAT 25-JUN-2003
LOCUS		
DEFINITION		Sequence 2918 from Patent WO03040369.
ACCESSION		AX759597
VERSION		AX759597.1 GI:32254213
KEYWORDS		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1
TITLE		Teleman, A., Anson, R. and Tuijinder, M.
JOURNAL		Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
FEATURES		Patent: WO 03040369-A 2918 15-MAY-2003;
source		Molecular Engines Laboratories (FR)
		Location/Qualifiers
		1. .17
		/organism="Homo sapiens"
		/mol_type="unassigned DNA"
		/db_xref="taxon:9606"
Query Match		0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity		88.2%; Pred. No. 1e+02;
Matches	15; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	717	GAGTACTTCCAGGAC 733
DB	17	GAGAACTTCCAGGATC 1
RESULT 153		
AX759648/C		17 bp DNA linear PAT 25-JUN-2003
LOCUS		
DEFINITION		Sequence 2969 from Patent WO03040369.
ACCESSION		AX759648
VERSION		AX759648.1 GI:32254264
KEYWORDS		Homo sapiens (human)
SOURCE		Homo sapiens
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1
TITLE		Teleman, A., Anson, R. and Tuijinder, M.
JOURNAL		Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
FEATURES		Patent: WO 03040369-A 2969 15-MAY-2003;
source		Molecular Engines Laboratories (FR)
		Location/Qualifiers
		1. .17
		/organism="Homo sapiens"
		/mol_type="unassigned DNA"
		/db_xref="taxon:9606"
Query Match		0.9%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. le+02; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0;

QY 902 CTCCTATCTGGGATC 918
 |||||
 Db 17 CTCCTGTCGGGATC 1

RESULT 154
 AX783524/c
 LOCUS AX783524 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Sequence 1855 from Patent WO03050284.
 ACCESSION AX783524
 VERSION AX783524.1 GI:32951373
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Guo, J.
 HUMAN prostate cancer candidate protein 1
 TITLE Human prostate cancer candidate protein 1
 JOURNAL Patent: WO 03050284-A 1855 19-JUN-2003;
 Amersham Biosciences (SV) Corp. (US)
 FEATURES
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. le+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

QY 1508 GGAGGAGAGCCAGAG 1524
 |||||
 Db 17 GGAGGAGAGCCAGAG 1

RESULT 155
 AX783525/c
 LOCUS AX783525 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Sequence 1856 from Patent WO03050284.
 ACCESSION AX783525
 VERSION AX783525.1 GI:32951374
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Guo, J.
 HUMAN prostate cancer candidate protein 1
 TITLE Human prostate cancer candidate protein 1
 JOURNAL Patent: WO 03050284-A 1856 19-JUN-2003;
 Amersham Biosciences (SV) Corp. (US)
 FEATURES
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. le+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

QY 1507 AGGAGGAGAGCCAGAA 1523
 |||||
 Db 17 AGGAGGAGAGCCAGCA 1

RESULT 156
 AX784014/c
 LOCUS AX784014 17 bp DNA linear PAT 17-JUL-2003

DEFINITION Sequence 2345 from Patent WO03050284.
 ACCESSION AX784014
 VERSION AX784014.1 GI:32951863
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Guo, J.
 HUMAN prostate cancer candidate protein 1
 TITLE Human prostate cancer candidate protein 1
 JOURNAL Patent: WO 03050284-A 2345 19-JUN-2003;
 Amersham Biosciences (SV) Corp. (US)
 FEATURES
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. le+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

QY 1504 CCAAGGAGGAGCAACCA 1520
 |||||
 Db 17 CCAAGGAGGAGCAACCA 1

RESULT 157
 AX784015/c
 LOCUS AX784015 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Sequence 2346 from Patent WO03050284.
 ACCESSION AX784015
 VERSION AX784015.1 GI:32951864
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Guo, J.
 HUMAN prostate cancer candidate protein 1
 TITLE Human prostate cancer candidate protein 1
 JOURNAL Patent: WO 03050284-A 2346 19-JUN-2003;
 Amersham Biosciences (SV) Corp. (US)
 FEATURES
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. le+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

QY 1503 ACCAAGGAGGAGCAACC 1519
 |||||
 Db 17 ACCAAGGAGGAGCAACC 1

RESULT 158
 AX784016/c
 LOCUS AX784016 17 bp DNA linear PAT 17-JUL-2003
 DEFINITION Sequence 2347 from Patent WO03050284.
 ACCESSION AX784016
 VERSION AX784016.1 GI:32951865
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 Guo, J.
 HUMAN prostate cancer candidate protein 1
 TITLE Human prostate cancer candidate protein 1

```

JOURNAL Patent: WO 03050284-A 2347 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
  Location/Qualifiers
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1502 AACCAAGGAGGAGGAGC 1518
Db 17 AACCAAGGAGGAGGAGC 1

RESULT 159
BD104867/c
LOCUS
DEFINITION
  Kit and method for determining HLA type.
ACCESSION
  BD104867
VERSION
  BD104867.1 GI:22650441
KEYWORDS
  WO 0192572-A/971.
SOURCE
  synthetic construct
  artificial construct
  artificial sequences.
REFERENCE
  1 (bases 1 to 17)
AUTHORS
  Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
  Nishida,M.
TITLE
  Kit and method for determining HLA type
JOURNAL
  Patent: WO 0192572-A 971 06-DEC-2001;
  NISHIHINO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
  KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
  NISHIDA
COMMENT
  OS Artificial Sequence
  PN WO 0192572-A/971
  PD 06-DEC-2001
  PF 01-JUN-2001 WO 2001JP004662
  PR 01-JUN-2000 JP 00P 164798
  PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI
  MATSUMURA,
  PI SHOGO MORIYA,MICHIO NISHIDA
  PC C1201/68 C12M1/00,C12N15/09,G01N33/53
  CC Description of Artificial Sequence,capture
  FH Key Location/Qualifiers
  FT source
  FT source
  Location/Qualifiers
    1. .17
    /organism="Artificial Sequence"
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match
  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CACTCGGTCTATCCTGAG 54
Db 17 CACTCGGTCTATCCTGTG 1

RESULT 160
BD197713/c
LOCUS
DEFINITION
  Method and reagent for treating diseases or conditions concerning
  molecule participating in vasculogenic response.
ACCESSION
  BD197713
VERSION
  BD197713.1 GI:33007483
KEYWORDS
  JP 2002509721-A/739.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 17)
      Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
      Method and reagent for treating diseases or conditions concerning
      molecule participating in vasculogenic response
      Patent: JP 2002509721-A 739 02-APR-2002;
      RIBOZYME PHARMACEUTICALS INC
      OS Homo sapiens (human)
      PN JP 2002509721-A/739
      PD 02-APR-2002
      PF 24-MAR-1999 JP 2000541291
      PR 27-MAR-1998 US 60/079678
      PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
      PI JAMES A MCSWIGGEN
      PC C12N15/09,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
      A61P29/00
      PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
      C12N5/00
      CC Method and reagent for treating diseases or conditions CC
      concerning molecule
      CC participating in vasculogenic response
      FH Key Location/Qualifiers
      FT source
      FT source
      Location/Qualifiers
        1. .17
        /organism="Homo sapiens"
        /mol_type="genomic RNA"
        /db_xref="taxon:9606"

Query Match
  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1375 ATTCTGAAGAGGAGGGA 1391
Db 17 ATTCTGAAGAGGAGGGA 1

RESULT 161
AR435876/c
LOCUS
DEFINITION
  Sequence 135 from patent US 6656731.
ACCESSION
  AR435876
VERSION
  AR435876.1 GI:40198960
KEYWORDS
  Unknown.
SOURCE
  Unknown.
  ORGANISM
    Unclassified.
  1 (bases 1 to 16)
  Eckstein,F., Ludwig,J. and Beigelman,L.
  Nucleic acid catalysts with endonuclease activity
  Patent: US 6656731-A 135 02-DEC-2003;
  JOURNAL
  LOCATION/Qualifiers
  FEATURES
    source
    Location/Qualifiers
      1. .16
      /organism="unknown"
      /mol_type="unassigned RNA"

Query Match
  0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 98;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 321 GACTACATTAAATTC 335
Db 16 GACTACATTAAATTC 2

RESULT 162
AR043790
LOCUS
DEFINITION
  Sequence 160 from patent US 5814517.

```

Query Match	0.8%; Score 13; DB 1; Length 14;
Best Local Similarity	100.0%; Pred. No. 83;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 721 ACTTCCCAGGAAC 733	
Db 1 ACTTCCCAGGAAC 13	
RESULT 165	
A58492	15 bp DNA linear PAT 05-MAR-1998
LOCUS	
DEFINITION	Sequence 2 from Patent WO9637605.
ACCESSION	A58492
VERSION	A58492.1 GI:3714127
KEYWORDS	
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1
TITLE	Pirotzky, E. and Colote, S.
JOURNAL	ANTI SENSE OLIGONUCLEOTIDES FOR BLOCKING IGE RECEPTOR SYNTHESIS
COMMENT	Patent: WO 9637605-A 2 28-NOV-1996;
FEATURES	SOD CONSEILS RECH APPLIC (FR)
source	Other publication AU 6008296 961211.
	Location/Qualifiers
	1..15
	/organism="unidentified"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32644"
Query Match	0.8%; Score 13; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 853 TAATGGAGATGTT 865	
Db 1 TAATGGAGATGTT 13	
RESULT 166	
A58495	15 bp DNA linear PAT 05-MAR-1999
LOCUS	
DEFINITION	Sequence 5 from Patent WO9637605.
ACCESSION	A58495
VERSION	A58495.1 GI:3714130
KEYWORDS	
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1
TITLE	Pirotzky, E. and Colote, S.
JOURNAL	ANTI SENSE OLIGONUCLEOTIDES FOR BLOCKING IGE RECEPTOR SYNTHESIS
COMMENT	Patent: WO 9637605-A 5 28-NOV-1996;
FEATURES	SOD CONSEILS RECH APPLIC (FR)
source	Other publication AU 6008296 961211.
	Location/Qualifiers
	1..15
	/organism="unidentified"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32644"
Query Match	0.8%; Score 13; DB 1; Length 15;
Best Local Similarity	100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 853 TAATGGAGATGTT 865	
Db 1 TAATGGAGATGTT 13	
RESULT 167	
A88175/c	

LOCUS A88175 15 bp DNA linear PAT 23-JAN-2000
DEFINITION Sequence 323 from Patent WO9833904.
ACCESSION A88175
VERSION A88175.1 GI:6736745
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 323 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers
source
1..15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1377 TCTGAAGAGGAGG 1389
Db 13 TCTGAAGAGGAGG 1
RESULT 168
A90142/c
LOCUS A90142 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 323 from Patent EP0856579.
ACCESSION A90142
VERSION A90142.1 GI:6738656
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 323 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source
1..15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1377 TCTGAAGAGGAGG 1389
Db 13 TCTGAAGAGGAGG 1
RESULT 169
AR070443
LOCUS AR070443 15 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5892023.
ACCESSION AR070443
VERSION AR070443.1 GI:7221331
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pirotzky,E. and Colote,S.
TITLE Anti sense oligonucleotides for blocking IGE receptor synthesis
JOURNAL Patent: US 5892023-A 2 06-APR-1999;
FEATURES Location/Qualifiers

source
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 853 TAATGGAGATGTT 865
Db 1 TAATGGAGATGTT 13
RESULT 170
AR070446
LOCUS AR070446 15 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5892023.
ACCESSION AR070446
VERSION AR070446.1 GI:7221334
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pirotzky,E. and Colote,S.
TITLE Anti sense oligonucleotides for blocking IGE receptor synthesis
JOURNAL Patent: US 5892023-A 5 06-APR-1999;
FEATURES Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 853 TAATGGAGATGTT 865
Db 1 TAATGGAGATGTT 13
RESULT 171
161704
LOCUS 161704 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 258 from patent US 5658780.
ACCESSION 161704
VERSION 161704.1 GI:2479652
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 258 19-AUG-1997;
FEATURES Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1045 GGACATATGAGAC 1057
Db 2 GGACATATGAGAC 14
RESULT 172
AR180305
LOCUS AR180305 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 373 from patent US 6333152.

```

ACCESSION   AR180305
VERSION     AR180305.1  GI:20222338
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS    Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE      Gene expression profiles in normal and cancer cells
JOURNAL    Patent: US 633152-A 373 25-DEC-2001;
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="unknown"
               /mol_type="unassigned DNA"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 513 TGGGCTGGGGGCC 525
Db 3 TGGGCTGGGGGCC 15

RESULT 173
LOCUS       AX572210 15 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 250 from Patent WO02055741.
ACCESSION   AX572210
VERSION     AX572210.1 GI:26004300
KEYWORDS    Human immunodeficiency virus
ORGANISM    Human immunodeficiency virus
SOURCE      Viruses; Retroviridae; Lentivirus; Primate
             lentivirus group.
REFERENCE   1
AUTHORS    de Smet,K. and Stuyver,L.
TITLE      Method for detection of drug-induced mutations in the hiv reverse
             transcriptase gene
JOURNAL    Patent: WO 02055741-A 250 18-JUL-2002;
             INNOGENETICS N.V. (BE)
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="Human immunodeficiency virus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:12721"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1273 CCATCCCTGAGGA 1285
Db 15 CCATCCCTGAGGA 3

RESULT 174
LOCUS       AX636172 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 3311 from Patent EP1260586.
ACCESSION   AX636172
VERSION     AX636172.1 GI:28471786
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS    Stinchcomb,D.T., Dudyycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
             Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
             Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
             Svedler,D., Thompson,J.D., Tracz,D., Usman,N., Mincott,F.E. and
             Wolf,T.
TITLE      Method and reagent for inhibiting the expression of disease related

```

```

Genes
Patent: EP 1260586-A 3311 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
             source
               1..15
               /organism="unidentified"
               /mol_type="unassigned RNA"
               /db_xref="taxon:32644"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1045 GGACATATGAGAC 1057
Db 2 GGACATATGAGAC 14

RESULT 175
LOCUS       BD065688/c 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION   BD065688
VERSION     BD065688.1 GI:22611291
KEYWORDS    JP 2001511000-A/323.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 15)
AUTHORS    Schlingensiepen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 323 07-AUG-2001;
             BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
             OS Unknown
             PN JP 2001511000-A/323
             PD 07-AUG-2001
             PF 30-JAN-1998 JP 1998532533
             PR 31-JAN-1997 EP 97101531.8
             PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
             PC C12N15/11,C07H21/04,A51K31/70
             CC An antisense oligonucleotide preparation method FH Key
             Location/Qualifiers
             FT source
               1..15
               /organism="Unknown".
             FT Location/Qualifiers
               1..15
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"
Query Match      0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1377 TCTGAAGAGGAGG 1389
Db 13 TCTGAAGAGGAGG 1

RESULT 176
LOCUS       AR010015 16 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 27 from patent US 5756684.
ACCESSION   AR010015
VERSION     AR010015.1 GI:3968820
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Johnson,E.M. and Bergemann,A.D.
TITLE      Cloning and expression of PUR protein
JOURNAL    Patent: US 5756684-A 27 26-MAY-1998;

```

```
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
    0.8%; Score 13; DB 1; Length 16;
  Best Local Similarity
    100.0%; Pred. No. 1.1e+02;
  Matches
    13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1383 GAGGAGGGAGG 1395
Db 2 GAGGAGGGAGG 14

RESULT 177
AR034750
LOCUS AR034750 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 27 from patent US 5869622.
ACCESSION AR034750
VERSION AR034750.1 GI:5950355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Johnson,E.M. and Bergemann,A.D.
TITLE Monoclonal antibodies to the pur protein
JOURNAL Patent: US 5869622-A 27 09-FEB-1999;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
    0.8%; Score 13; DB 1; Length 16;
  Best Local Similarity
    100.0%; Pred. No. 1.1e+02;
  Matches
    13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1383 GAGGAGGGAGG 1395
Db 2 GAGGAGGGAGG 14

RESULT 178
AR096597/c
LOCUS AR096597/c 16 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 27 from patent US 6008045.
ACCESSION AR096597
VERSION AR096597.1 GI:10025536
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Copeland,W.C. and Wang,T.S.-F.
TITLE Nucleic acid encoding human DNA polymerase .alpha
JOURNAL Patent: US 6008045-A 27 28-DEC-1999;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
    0.8%; Score 13; DB 1; Length 16;
  Best Local Similarity
    100.0%; Pred. No. 1.1e+02;
  Matches
    13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CTCTGCCCGCTGG 24
Db 16 CTCTGCCCGCTGG 4

RESULT 179
AR105973/c
LOCUS AR105973 16 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 27 from patent US 6103473.
ACCESSION AR105973
VERSION AR105973.1 GI:12820038
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 16)
AUTHORS Copeland,W.C. and Wang,T.S.-F.
TITLE Mutagenicity screening method using human DNA polymerase or catalytic polypeptide
JOURNAL Patent: US 6103473-A 27 15-AUG-2000;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
    0.8%; Score 13; DB 1; Length 16;
  Best Local Similarity
    100.0%; Pred. No. 1.1e+02;
  Matches
    13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CTCTGCCCGCTGG 24
Db 16 CTCTGCCCGCTGG 4

RESULT 180
AX327134/c
LOCUS AX327134/c 16 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 330 from Patent WO0178894.
ACCESSION AX327134
VERSION AX327134.1 GI:18097846
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1
AUTHORS Keith,T.
TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
JOURNAL Patent: WO 0178894-A 330 25-OCT-2001;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Primer"

  Query Match
    0.8%; Score 13; DB 1; Length 16;
  Best Local Similarity
    100.0%; Pred. No. 1.1e+02;
  Matches
    13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 AGGACTGTCCAGT 415
Db 13 AGGACTGTCCAGT 1

RESULT 181
AI8727/c
LOCUS AI8727 16 bp DNA linear PAT 18-APR-1994
DEFINITION kozak consensus leader sequence.
ACCESSION AI8727
VERSION AI8727.1 GI:513378
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1 (bases 1 to 16)
AUTHORS Peakman,T.C., Page,M.J. and Charles,I.G.
TITLE Baculoviral expression system comprising procaryotic leader sequence
JOURNAL Patent: EP 0486170-A 2 20-MAY-1992;
```



```

THE WELLCOME FOUNDATION LIMITED
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 644 CCATGCTGACGGCGTG 659
Db 16 CCATGCTGCGCGCGG 1

RESULT 182
LOCUS A29549 16 bp DNA linear PAT 12-JUN-1995
DEFINITION Oligonucleotide probe.
ACCESSION A29549
VERSION A29549.1 GI:1248955
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Mackellar,W.C. and Robey,C.S.
TITLE An improved method for folding tissue plasminogen activators and
JOURNAL derivatives thereof
JOURNAL Patent: EP 0523296-A 18 20-JAN-1993;
ELI LILLY AND COMPANY
FEATURES
source
1..16
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 464 GGCAAGTGTCTGAAA 479
Db 1 GCGAAGTCTGTGAAA 16

RESULT 183
LOCUS A42606 16 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 124 from Patent WO9502051.
ACCESSION A42606
VERSION A42606.1 GI:2398055
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND
CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 124 19-JAN-1995;
BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT Other publication AU 7345694 950206.
FEATURES
source
1..16
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.8%; Score 12.8; DB 1; Length 16;

THE WELLCOME FOUNDATION LIMITED
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 715 GAGAGTACTTCCGAGG 730
Db 1 GAGAGTACTTCTTAGG 16

RESULT 184
LOCUS A88795 16 bp DNA linear PAT 29-JAN-2000
DEFINITION Sequence 943 from Patent WO9833904.
ACCESSION A88795
VERSION A88795.1 GI:6737365
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 943 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1..16
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 715 GAGAGTACTTCCGAGG 730
Db 1 GAGAGTACTTCTTAGG 16

RESULT 185
LOCUS AR072525 16 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 22 from patent US 5948616.
ACCESSION AR072525
VERSION AR072525.1 GI:9999289
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Chao,L. and Chao,J.
TITLE Methods and compositions of correlating tissue kallikrein gene
promoter polymorphisms with essential hypertension
JOURNAL Patent: US 5948616-A 22 07-SEP-1999;
FEATURES
source
1..16
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1385 GGAGGGAGAGGGGGGC 1400
Db 1 GGAGGGGGGGGGGGGC 16

RESULT 186
LOCUS BD244651 16 bp DNA linear PAT 17-JUL-2003
DEFINITION Low temperature-adaptable equine influenza virus.
ACCESSION BD244651
VERSION BD244651.1 GI:33054421

```



```
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 11 26-NOV-2002;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="genomic DNA"
Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1184 CCTGAGAGATCAAA 1199
Db 1 CCAGCAGAAGATCAAA 16
RESULT 191
AR328586
LOCUS AR328586 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5988 from patent US 6566127.
ACCESSION AR328586
VERSION AR328586.1 GI:33714394
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5988 20-MAY-2003;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned RNA"
Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 466 CAAGTCCTCTGAACT 481
Db 1 CAACTGCTTTGAACT 16
RESULT 192
AR343259
LOCUS AR343259 16 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 35 from patent US 6579528.
ACCESSION AR343259
VERSION AR343259.1 GI:33738777
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Dowling,P.W. and Youngner,J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6579528-A 35 17-JUN-2003;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="genomic DNA"
Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 556 GCTTCCTCTTACGTCAA 571
Db 1 GCATCTGTTAAGTCAA 16
```

```
RESULT 193
AR367752
LOCUS AR367752 16 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 22 from patent US 6376182.
ACCESSION AR367752
VERSION AR367752.1 GI:34601131
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Chao,L., Chao,J. and Song,O.
TITLE Methods and compositions for correlating tissue kallikrein gene promoter polymorphisms with treatment of essential hypertension
JOURNAL Patent: US 6376182-A 22 23-APR-2002;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="genomic DNA"
Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1385 GGAGGGAGAGGGGGC 1400
Db 1 GGAGGGGGGGGGGGC 16
RESULT 194
BD066308
LOCUS BD066308 16 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066308
VERSION BD066308.1 GI:22611911
KEYWORDS JP 2001511000-A/943.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 943 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MEH
  OS Unknown
  PN JP 2001511000-A/943
  PD 07-AUG-2001
  PF 30-JAN-1998 JP 1998532533
  PR 31-JAN-1997 EP 9710131.8
  PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
  PC C12N15/11,C07H21/04,A61K31/70
  CC An antisense oligonucleotide preparation method FH Key
  Location/Qualifiers
    FT source
      1..16
      /organism='Unknown'
      /organism='Unknown'
      Location/Qualifiers
        1..16
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
Query Match
  Best Local Similarity 0.8%; Score 12.8; DB 1; Length 16;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 715 GAGAGTACTTCCAGG 730
Db 1 GAGAGTACTTCTAGG 16
Search completed: June 24, 2004, 09:51:26
```

lacourciere538-2.rge

Thu Jun 24 10:30:08 2004

Job time : 8 secs